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Sequence Listing

TECH CENTER 1600/2900

<110> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.

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B1



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Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln  
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Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr  
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 tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag 250  
 aacttttgat aaaaagggat ttcattgaat cgctgcctgt ctgactgaat 300  
 caggatcaac agcttttaaag gcagaaacct cagagagact tcgtactgtg 350  
 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400  
 gaagaaccaa gttggggaga aaggtctctg gggctctgatc aataatgctg 450  
 gtgttcccg cgtgctggct cccactgact ggctgacact agaggactac 500  
 agagaaccta ttgaagtga cctgtttgga ctcatcagtg tgacactaaa 550  
 tatgcttctt ttggtcaaga aagctcaagg gagagtatt aatgtctcca 600  
 gtgttgagg tcgccttgca atcgttggag ggggtatac tccatccaaa 650  
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 tgggtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750  
 cagatccagt aaaggtatt gaaaaaaaaac tcgccatttg ggagcagctg 800  
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 agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900  
 tggtagagt catggaccac gctctaaca gtctcttccc taagactcat 950  
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 ctttgaaaag gagggctgga atggtacatc acataggcaa gtccctgccct 1300  
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 gccattcaa aatgatcttt accgtggcct gcccattgct tatggtcccc 1400  
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 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

B1

aaaaaaaa 1508

<210> 10  
<211> 319  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-17  
<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 36-47, 108-113, 166-171,198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature  
<222> 39-42  
<223> Glycosaminoglycan Attachment Site.

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<220>  
<221> TRANSMEM  
<222> 136-152  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 161-163, 187-190 and 253-256  
<223> N-glycosylation Sites.

<400> 10  
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu  
1 5 10 15  
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys  
20 25 30  
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45  
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60  
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75  
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90  
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105  
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120



Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu  
 125 130 135  
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro  
 140 145 150  
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val  
 155 160 165  
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys  
 170 175 180  
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys  
 185 190 195  
 Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys  
 200 205 210  
 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala  
 215 220 225  
 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu  
 230 235 240  
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser  
 245 250 255  
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His  
 260 265 270  
 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys  
 275 280 285  
 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala  
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 Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn  
 305 310 315  
 Pro Lys Ala Val

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

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 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300  
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
 gggttaaaac cagcaaattc acccgtotta ccagctcctc agaaggcgga 450  
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600  
 ggatccccgc ccggaaggag atccgcagag gacagtcatc agctggaggg 650  
 gagcggatg cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750  
 agtgcatctg aactatcgcc agaagggcgt gattgacgtc ttctgcatg 800  
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
 gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900  
 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950  
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 aacctgtttg agagcacgat ccgcactctg ggggggctcc tgagtgccta 1050  
 ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100  
 atcggctaata gcctgccttc agaacaccat ccaagattcc ttactcgat 1150  
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 ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450  
 gggaaacagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500  
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 tgggggagct tgcccacggc cgcttcagt ccaagatgga ccacctggtg 1600  
 tgcttctgc cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650

B1

cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
 accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750  
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 caacctgctg cggccagaga ccgtggagag cctgtttctac ctgtaccgcg 1850  
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900  
 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950  
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
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 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100  
 gcctatctgg acccctgcct aggggtgatg gctgctggtg tggggacttc 2150  
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 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250  
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 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
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 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450  
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctgaagc 2500  
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 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
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 ttgatttgct ctaaccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala	20	25	30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro	35	40	45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr	50	55	60
Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp	65	70	75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu	80	85	90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala	95	100	105
Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile			

B1

B1

	290		295		300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser		
	305	310	315		
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu		
	320	325	330		
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu		
	335	340	345		
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn		
	350	355	360		
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser		
	365	370	375		
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr		
	380	385	390		
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe		
	395	400	405		
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala		
	410	415	420		
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys		
	425	430	435		
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe		
	440	445	450		
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr		
	455	460	465		
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu		
	470	475	480		
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg		
	485	490	495		
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val		
	500	505	510		
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu		
	515	520	525		
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly		
	530	535	540		
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr		
	545	550	555		
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu		
	560	565	570		
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val		

575                                      580                                      585  
 Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr  
    590                                      595                                      600  
 Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys  
    605                                      610                                      615  
 Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe  
    620                                      625                                      630  
 Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln  
    635                                      640                                      645  
 Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe  
    650                                      655                                      660  
 Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp  
    665                                      670                                      675  
 Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala  
    680                                      685                                      690  
 His Pro Leu Pro Ile Trp Thr Pro Ala  
    695

<210> 13  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 13  
 cgccagaagg gcgtgattga cgtc 24

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 14  
 ccatccttct tcccagacag gccg 24

<210> 15  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150  
ccctcggaag tgttcctct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250  
cgggcagtcg ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
cccaccgcct ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400  
ctgggtcttcg tgccccacat gcgcgcgttc ctgagcagga agaagatccg 450  
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500  
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tggtcttctc gaggtgggc ccttcacgt ggctccccg gagctccacc 650  
ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700  
cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750  
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atgtggagtg gccaggacca agacagcaag ctacgaatt gcagccacc 1200  
ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250

B1

cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300  
 cgggaccccc cctgccttcc tgctcacctt actctgacct ccttcacgtg 1350  
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 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450  
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
 20 25 30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
 35 40 45

B1



Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
 50 55 60  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
 65 70 75  
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
 80 85 90  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
 95 100 105  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
 110 115 120  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
 125 130 135  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu  
 140 145 150  
 Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp  
 155 160 165  
 Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala  
 170 175 180  
 Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His  
 185 190 195  
 Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His  
 200 205 210  
 Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly  
 215 220 225  
 Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu  
 230 235 240  
 Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe  
 245 250 255  
 Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg  
 260 265 270  
 Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly  
 275 280 285  
 Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu  
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 Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp  
 305 310 315  
 Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser  
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B1

<210> 18  
<211> 23  
<212> DNA  
<<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 18  
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<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
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aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150  
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagatagga acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtgg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18  
<223> Growth factor and cytokines receptors family.

B1  
<400> 22  
Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly  
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Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30  
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45  
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60  
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23  
<211> 2883  
<212> DNA  
<213> Homo sapiens

<400> 23  
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ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150  
ggctccgggg cggcccgcta ggccagtgcg ccgcgcgtcg cccgcaggc 200  
ccgggccgc agcatggagc caccggagc cggcggggc cgcgcgcagc 250  
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B1

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<211> 616

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-33

<223> Signal peptide.

<220>

<221> TRANSMEM

<222> 13-40

<223> Transmembrane domain (type II).

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35 40 45

Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
50 55 60

Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
65 70 75

Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser  
95 100 105

Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile  
110 115 120

Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp  
125 130 135

Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg  
140 145 150

Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe  
155 160 165

Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg  
170 175 180

Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile  
185 190 195

Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg  
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Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val  
215 220 225

Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu  
230 235 240

Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe  
245 250 255

Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp  
260 265 270

Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu  
275 280 285

B1

Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His	
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				305					310					315	
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	
				320					325					330	
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	
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Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	
				365					370					375	
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro	
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Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe	
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Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val	
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Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr	
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Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu	
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Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu	
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Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys	
				470					475					480	
Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu	
				485					490					495	
Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala	
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg	
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Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile	
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Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met	
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly	
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B1

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys  
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu  
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr  
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<210> 26  
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<212> DNA  
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<210> 27  
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<213> Homo sapiens

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gcagaggctt cgtgaaggag ttatcagaga cattgagagg caaattcgga 150



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 35 40 45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
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 <212> DNA  
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<400> 30

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 <212> PRT  
 <213> Homo sapiens

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 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
 65 70 75  
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
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 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
 95 100 105

Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr  
110 115 120

Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp  
125 130 135

His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala  
140 145 150

Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile  
155 160 165

Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
170 175 180

Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
185 190 195

Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr  
200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu  
215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu  
245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln  
260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr  
275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr  
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<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg  
 125 130 135  
 Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys  
 140 145 150  
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 155 160 165  
 Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala  
 170 175 180  
 Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly  
 185 190 195  
 His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu  
 200 205 210  
 Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser  
 215 220 225  
 Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu  
 230 235 240  
 Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro  
 245 250 255  
 Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala  
 260 265 270  
 Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser  
 275 280 285  
 Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu  
 290 295 300  
 Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser  
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 Glu Pro Glu Glu Gln  
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<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

tgctctttgt cccagacttc tgtcc 25



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<210> 36  
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<400> 37  
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<210> 38  
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<220>  
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<210> 39  
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<212> DNA  
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<400> 39  
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<210> 40  
<211> 2084

B1

<212> DNA  
<213> Homo sapiens

<400> 40

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B1

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<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
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Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
 110 115 120  
 Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
 125 130 135  
 Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
 140 145 150  
 Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
 155 160 165  
 Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
 170 175 180  
 Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
 185 190 195  
 Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu  
 200 205 210  
 Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn  
 215 220 225  
 Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe  
 230 235 240  
 Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu  
 245 250 255  
 Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser  
 260 265 270  
 His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu  
 275 280 285  
 Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser  
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 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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tgtgtaggtg ctgaatgctg taaggagttt aggttgatg aattctacaa 1550

ccctataata aattttactc tatacaaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
35 40 45

Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu  
50 55 60

Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr  
65 70 75

Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys  
80 85 90

Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu  
95 100 105

Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp  
110 115 120

Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp  
125 130 135

Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr  
140 145 150

Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu  
155 160 165

Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe  
170 175 180

Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val  
185 190 195

Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn  
200 205 210

Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe  
215 220 225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

B1

230

235

240

Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile  
245 250 255

Val Glu Thr Lys Ile Cys Gln Glu  
260

&lt;210&gt; 44

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 44

gaaagacacg acacagcagc ttgc 24

&lt;210&gt; 45

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 45

gggaactgct atctgatgcc 20

&lt;210&gt; 46

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 46

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&lt;210&gt; 47

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 47

cttctcgaac cacataagtt tgaggcag 28

&lt;210&gt; 48

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

B1

<220>

<223> Synthetic oligonucleotide probe

<400> 48

cacgattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600

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agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850

cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900

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B1



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 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950  
 aaaaaaaaaa aaaaaaaga 1969

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
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 20 25 30  
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
 35 40 45  
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
 50 55 60  
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
 65 70 75  
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

	80	85	90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala	95	100	105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln	110	115	120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys	125	130	135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe	140	145	150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala	155	160	165
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr	170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp	185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys	200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro	215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu	230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly	245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro	260	265	270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val	275	280	

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 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

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 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200  
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 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450  
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 tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750  
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<212> PRT

<213> Homo sapiens

<400> 52

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Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly  
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Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr  
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Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly  
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Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala  
95 100 105

Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val  
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Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val  
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Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile  
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Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro  
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Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln  
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Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly  
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 Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu  
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 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr  
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 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser  
 65 70 75  
 Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys  
 80 85 90  
 Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln  
 95 100 105  
 Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His  
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 Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu  
 125 130 135  
 Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val  
 140 145 150



Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu  
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Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu  
170 175 180

Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala  
185 190 195

Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg  
200 205 210

Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala  
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Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp  
230 235 240

Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala  
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Arg Gly Glu Arg Arg Gly Cys Ser Arg Ala  
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<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg Ser Arg Arg  
 35 40 45

Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro  
 50 55 60

Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val  
 65 70 75

Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro  
 80 85 90

Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro  
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Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg  
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Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln  
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Glu Phe Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly  
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Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val  
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Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala

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Glu Thr Gly Lys	Asp Arg Glu Lys Ser	His Ser Trp Leu Ser	Thr
	200	205	210
Gly Trp Phe Thr	Met Val Ile Ala Val	Glu Leu Cys Asp His	Val
	215	220	225
His Val Tyr Gly	Met Val Pro Pro Asn	Tyr Cys Ser Gln Arg	Pro
	230	235	240
Arg Leu Gln Arg	Met Pro Tyr His Tyr	Tyr Glu Pro Lys Gly	Pro
	245	250	255
Asp Glu Cys Val	Thr Tyr Ile Gln Asn	Glu His Ser Arg Lys	Gly
	260	265	270
Asn His His Arg	Phe Ile Thr Glu Lys	Arg Val Phe Ser Ser	Trp
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 tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100  
 cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150  
 aataggggct gcccctcggc tgcagtgggc taccgggca tgaagcccca 3200  
 gcagcactgc ccaggcgagc ttcagcagca gactgacacc agcagcctgc 3250  
 tgaggcagac ccatcttggc aatggatatg acccccaaag tcaccagatc 3300  
 acgaggggtc ccaagtctag cccggacgag ggctctttct tatacacact 3350  
 gcccgacgac tccactcacc agctgctgca gcccacac gactgctgcc 3400  
 aacgccagga gcagcctgct gctgtgggcc agtcaggggt gaggagagcc 3450  
 cccgacagtc ctgtcctgga agcagtgtgg gacctccat ttcactcagg 3500

B1

gcccccatgc tgcttgggcc ttgtgccagt tgaagaggtg gacagtcttg 3550  
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 agagacagag aaaattggta tttatttttc tattatagcc atatttatat 3800  
 atttatgcac ttgtaaataa atgtatatgt ttataattc tggagagaca 3850  
 taaggagtcc taccggttga ggttgagag ggaaaataaa gaagctgcc 3900  
 cctaacagga gtcaccagg aaagcaccgc acaggctggc gcgggacaga 3950  
 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000  
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 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200  
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<210> 58  
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 <212> PRT  
 <213> Homo sapiens

<400> 58

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				20					25				30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
				35					40				45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
				50					55				60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
				65					70				75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
				80					85				90	

Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270
Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu	275	280	285
Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met	290	295	300
Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr	305	310	315
Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser	320	325	330
Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu	335	340	345
Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala	350	355	360
Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala	365	370	375

B1



Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	
				380					385					390	
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	
				395					400					405	
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	
				410					415					420	
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	
				425					430					435	
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	
				440					445					450	
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	
				455					460					465	
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	
				470					475					480	
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	
				485					490					495	
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	
				500					505					510	
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	
				515					520					525	
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	
				530					535					540	
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	
				545					550					555	
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg	
				560					565					570	
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln	
				575					580					585	
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp	
				590					595					600	
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile	
				605					610					615	
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg	
				620					625					630	
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys	
				635					640					645	
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile	
				650					655					660	

B1

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly	
				665					670					675	
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu	
				680					685					690	
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr	
				695					700					705	
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr	
				710					715					720	
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met	
				725					730					735	
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr	
				740					745					750	
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys	
				755					760					765	
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His	
				770					775					780	
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn	
				785					790					795	
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr	
				800					805					810	
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro	
				815					820					825	
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	
				830					835					840	
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	
				845					850					855	
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	

B1

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu  
 950 955 960  
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His  
 965 970 975  
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly  
 980 985 990  
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro  
 995 1000 1005  
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys  
 1010 1015 1020  
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg  
 1025 1030 1035  
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro  
 1040 1045 1050  
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu  
 1055 1060 1065  
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp  
 1070 1075 1080  
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly  
 1085 1090 1095  
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr  
 1100 1105 1110  
 Pro Pro Leu Thr Ile  
 1115

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 <210> 60  
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 <212> DNA  
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 <223> Synthetic oligonucleotide probe  
  
 <400> 60  
 gcacacgtag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial Sequence

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<400> 61  
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
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<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
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cacgggcccgc gaggggttccc gcgcgctcag ccggcggtat ctgcggcgctc 150  
tgctgtctcct gctactgctg ctgctgctgc ggcagcccgt aaccgcgcgcg 200  
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ctacgccagg caccccc aaa accctggacc ttcggggctc gcgcagggcc 350  
ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
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gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
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caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700  
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750  
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagtct 800  
agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850

B1

agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900  
 catcggacac cttgataaga agggtccttg aagtgtctca ggctcctgtg 950  
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000  
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 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
 cacatggaaa a 1661

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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> 196, 386  
 <223> unknown amino acid

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 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg  
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 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala  
 35 40 45  
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
 50 55 60

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
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Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	
				260					265					270	
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro	
				275					280					285	
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu	
				290					295					300	
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly	
				305					310					315	
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu	
				320					325					330	
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg	
				335					340					345	

B1

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp	350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu	380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val	410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser	425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val	440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala	455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro	470	475	480
Thr Phe Thr Gln Trp Leu Cys	485		

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 gtcacacaca gctctggcag ctgag 25  
  
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 <212> DNA  
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<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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ggcccagcaa gcctgataag catgaagctc ttatcttttg tggctgtggt 150  
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200  
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250  
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
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gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
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tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaagggtgc 600  
ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650  
atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
ctccttctcc ctaacttttag aaatgttgta cttggctatt ttgattaggg 850  
aagagggatg tggctctctga tctctgttgt cttcttgggt ctttggggtt 900  
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cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100  
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B1



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 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300  
 ctctgctgcc ggtccccctca cctgcacttg aggggtctgg gcagtccctc 1350  
 ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
 gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttggggt 1450  
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
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<210> 68  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 68

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 20 25 30  
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 35 40 45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
 50 55 60  
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
 65 70 75  
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
 80 85 90  
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
 95 100 105  
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
 110 115 120  
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
 125 130 135  
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
 140 145 150  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
 155 160 165

B1

Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
				170					175					180

Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggtcctccc 150  
 tccctttgca ttcccacccc tccgggcttt gcgtcttctt ggggaccccc 200  
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250  
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300  
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 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550  
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 ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050  
 catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100

B1

gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
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 agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
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 aaaatactcc tagaataact tggtatacaa taggttctaa aaataaaatt 1450  
 gctaaacaag aatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
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B1

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agattgagtt tgagcctgta tatctattaa aaatttcaac ttccacata 2750  
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atataacaat tattatattt acaatttggt ttctgcaata tttttcttat 2950  
gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000  
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gcagaatata ttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
taagataaaa tctattaaat ttttctctc taaaaactga aaaaaaaaaa 3150  
aaaaaaaaa aaaaaaaaaa 3170

<210> 70  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 70  
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20 25 30  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
35 40 45  
Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
50 55 60  
Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
65 70 75  
Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
80 85 90  
His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
95 100 105  
Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
 125 130 135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
 140 145 150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
 155 160 165  
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
 170 175 180  
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
 185 190 195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
 200 205 210  
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
 215 220 225  
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
 230 235 240  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
 245 250 255  
 Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200  
 tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250  
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 agcaccagag ccaggcagtc actgttcctc ctccctgggtt ggagtccttt 700  
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
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 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
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 cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250  
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 ctgaaaaga 1809

<210> 72  
 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 72

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Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225  
Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys  
230 235 240  
Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala  
245 250 255  
Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser  
260 265 270  
Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser

B1

	275		280		285
Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln					
	290		295		300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn					
	305		310		315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr					
	320		325		330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg					
	335		340		345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp					
	350		355		360

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 73  
 aattcatggc aaatatttcc cttccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 74  
 tggtaaactg gcccaaactc gg 22

<210> 75  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 75  
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<210> 76  
 <211> 1989  
 <212> DNA  
 <213> Homo sapiens

B1



<400> 76

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tgactcagc ggtggaggag acggacgcg ggtgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200  
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B1

cagccccaaa actggggtca gcctcagggc aggagtccca ctccctccagg 1450  
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caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu	1	5	10	15
Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp	20	25	30	
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu	35	40	45	
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro	50	55	60	
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val	65	70	75	
Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His	80	85	90	
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His	95	100	105	
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg	110	115	120	
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro	125	130	135	

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu  
 140 145 150  
 Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp  
 155 160 165  
 Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu  
 170 175 180  
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala  
 185 190 195  
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser  
 200 205 210  
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val  
 215 220 225  
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln  
 230 235 240  
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu  
 245 250 255  
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu  
 260 265 270  
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn  
 275 280 285  
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg  
 290 295 300  
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu  
 305 310 315  
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp  
 320 325 330  
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys  
 335 340

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens

<400> 78  
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 cagtctccga gctgaccagg aggcaactgt tgagaagctg ctggaccgcc 150  
 cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

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 ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350  
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 cccaagatgc cagtgaacca cgtccatgcc cattccgtgc aaggcagata 1650

B1

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 <212> PRT  
 <213> Homo sapiens

<400> 79  
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 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg  
 35 40 45  
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
 50 55 60  
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
 65 70 75  
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
 80 85 90  
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
 95 100 105  
 Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val  
 110 115 120  
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val  
 125 130 135

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr  
 140 145 150  
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe  
 155 160 165  
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr  
 170 175 180  
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met  
 185 190 195  
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr  
 200 205 210  
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp  
 215 220 225  
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe  
 230 235 240  
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu  
 245 250 255  
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe  
 260 265 270  
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser  
 275 280 285  
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro  
 290 295 300  
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val  
 305 310 315  
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile  
 320 325 330  
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe  
 335 340 345  
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu  
 350 355 360  
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn  
 365 370 375  
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile  
 380 385 390  
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys  
 395 400 405  
 Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser  
 410 415 420

B1



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caagcgttgg gcggaggacc agcacagcca gggtagcttt gtggtacagc 1450  
cgccggcgct ctggcaaacc gaaaaggatg actggacggc cccttatggc 1500  
cgcctctact ttgccggcga gcacaccgcc taccgcacg gctgggtgga 1550

B1



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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84

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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165  
 Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195

B1

Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr  
200 205 210

Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala  
215 220 225

Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr  
230 235 240

Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp  
245 250 255

Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro  
260 265 270

Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala  
275 280 285

Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln  
290 295 300

Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala  
305 310 315

Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile  
320 325 330

Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg  
335 340 345

Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg  
350 355 360

Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn  
365 370 375

Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu  
380 385 390

Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala  
395 400 405

Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu  
410 415 420

Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp  
425 430 435

Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser  
440 445 450

Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu  
455 460 465

Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly  
470 475 480

B1

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
				545					550					555
Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
				560					565					

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
 cccctcgcga gggctctgaat ttctgtctgc tgttcacaaa gatgcttttt 250  
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 tctttgctca gaataggcca gaggatga tctccgaatt ggcttggtac 700  
 acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750  
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 cccccaaaaa ggcattgggt ctgataggga atgtagagaa aggcttcacc 850

B1

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 cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250  
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B1

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tattacagat aaaaaa 3316

<210> 86  
<211> 739  
<212> PRT  
<213> Homo sapiens

<400> 86  
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Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro  
20 25 30  
Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser

	35	40	45
Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile	50	55	60
Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys	65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg	80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val	95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn	110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu	125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu	140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys	155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His	170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala	185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr	200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu	215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile	230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu	245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro	260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu	275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe	290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys	305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr			

B1

320

325

330

His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val  
335 340 345

Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr  
350 355 360

Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val  
365 370 375

Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg  
380 385 390

Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro  
395 400 405

Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn  
410 415 420

Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val  
425 430 435

Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp  
440 445 450

Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu  
455 460 465

Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser  
470 475 480

Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val  
485 490 495

Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe  
500 505 510

Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu  
515 520 525

Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr  
530 535 540

Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn  
545 550 555

Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala  
560 565 570

Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp  
575 580 585

Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile  
590 595 600

Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu

B1

605	610	615
Asn Ile Tyr Asn Arg Ser Gln Pro Val	Leu Gln Ile Phe Val His	
620	625	630
Gly Glu Ser Leu Arg Ser Ser Leu Val	Gly Val Val Val Pro Asp	
635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala	Lys Leu Gly Val Lys Gly	
650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln	Val Val Arg Glu Ala Ile	
665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys	Glu Ser Gly Leu Lys Thr	
680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu	His Pro Glu Pro Phe Ser	
695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr	Leu Lys Ala Lys Arg Gly	
710	715	720
Glu Leu Ser Lys Tyr Phe Arg Thr Gln	Ile Asp Ser Leu Tyr Glu	
725	730	735
His Ile Gln Asp		

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 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
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 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200  
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 catactcca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250  
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 cccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950  
 catcggggcc tgtggagatt gtttcggaag aagaaccact tcctggtggt 2000

B1

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<210> 88  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
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 Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr  
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 35 40 45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
 50 55 60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
 80 85 90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
 95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
 110 115 120  
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
 125 130 135  
 Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp  
 140 145 150  
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn  
 155 160 165  
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu  
 170 175 180  
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser  
 185 190 195  
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp  
 200 205 210  
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His  
 215 220 225  
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu  
 230 235 240  
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His  
 245 250 255  
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser  
 260 265 270  
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr  
 275 280 285  
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu  
 290 295 300  
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu  
 305 310 315  
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro  
 320 325 330  
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met  
 335 340 345  
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro  
 350 355 360  
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser  
 365 370 375  
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val  
 380 385 390

B1

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe	395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr	410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly	440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys	455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg	470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val	485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly	500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val	515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala	530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu	545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr	560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp	575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp	590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe	605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro	620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu	635	640	645
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<210> 89

<211> 25

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe

<400> 89  
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<210> 90  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 90  
cctcaaccag gccacgggcc ac 22

<210> 91  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 91  
cccaggcaga gatgcagtac aggc 24

<210> 92  
<211> 26  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
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<210> 93  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
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<210> 94  
<211> 3037  
<212> DNA  
<213> Homo sapiens

B1

<400> 94

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ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200  
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cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500  
tcatgttgct ggtggaccag attggtaact cccatgtgca ttctactgac 550  
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B1

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tcagcagctg tggaaataaa gcttgtgagc cctctgctgg ccacagtga 2800

B1

gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850  
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ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95  
<211> 307  
<212> PRT  
<213> Homo sapiens

<400> 95

Met	Asp	Asp	Phe	Ile	Ser	Ile	Ser	Leu	Leu	Ser	Leu	Ala	Met	Leu	1	5	10	15
Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe	20	25	30	
Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	35	40	45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	50	55	60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	65	70	75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	80	85	90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	95	100	105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu	110	115	120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	125	130	135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	155	160	165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	170	175	180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	185	190	195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	

B)



Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
 215 220 225  
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val  
 230 235 240  
 Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu  
 245 250 255  
 Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly  
 260 265 270  
 His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg  
 275 280 285  
 Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile  
 290 295 300  
 Leu Ser Val Gly His Gln His  
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<210> 96  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 96  
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<210> 97  
 <211> 25  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 97  
 ctgtgctcat gttcatggac aactg 25

<210> 98  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 99  
 <211> 1429

<212> DNA  
<213> Homo sapiens

<400> 99

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B1

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro  
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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe  
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg  
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg  
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu  
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe  
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val  
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu  
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln  
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg  
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu  
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys  
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp  
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu  
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly  
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser

B1

230	235	240
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245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu		
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Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val		
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro		
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Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met		
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu		
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu		
395	400	

<210> 101  
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 <212> DNA  
 <213> Homo sapiens

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gcgcctcaag gccctcacca ctggctcaact gcctaccttt attgatgctg 450  
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B1

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B1

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 agtgtaataa aatgataata t 3671

<210> 102  
 <211> 1089  
 <212> PRT  
 <213> Homo sapiens

<400> 102

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				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
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B1

Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	
				200					205					210	
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	
				215					220					225	
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	
				230					235					240	
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met	
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Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr	
				260					265					270	
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp	
				275					280					285	
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu	
				290					295					300	
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro	
				305					310					315	
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu	
				320					325					330	
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	
				335					340					345	
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala	
				350					355					360	
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser	
				365					370					375	
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	
				380					385					390	
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	
				395					400					405	
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr	
				410					415					420	
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	
				425					430					435	
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	
				440					445					450	

B1



Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys  
 455 460 465  
 Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys  
 470 475 480  
 Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile  
 485 490 495  
 Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu  
 500 505 510  
 Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe  
 515 520 525  
 Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala  
 530 535 540  
 Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Phe  
 545 550 555  
 Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala  
 560 565 570  
 Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val  
 575 580 585  
 Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu  
 590 595 600  
 Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg  
 605 610 615  
 His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu  
 620 625 630  
 Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr  
 635 640 645  
 Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met  
 650 655 660  
 Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala  
 665 670 675  
 Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg  
 680 685 690  
 Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg  
 695 700 705  
 Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala  
 710 715 720  
 Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu  
 725 730 735

B1

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu  
 740 745 750  
 Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val  
 755 760 765  
 Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu  
 770 775 780  
 Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr  
 785 790 795  
 Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly  
 800 805 810  
 Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala  
 815 820 825  
 Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu  
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 Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile  
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 Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu  
 860 865 870  
 His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe  
 875 880 885  
 Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr  
 890 895 900  
 Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile  
 905 910 915  
 His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser  
 920 925 930  
 Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala  
 935 940 945  
 Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp  
 950 955 960  
 Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro  
 965 970 975  
 Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu  
 980 985 990  
 Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe  
 995 1000 1005  
 Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu  
 1010 1015 1020

B1

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg  
                   1025                                  1030                                  1035  
 Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe  
                   1040                                  1045                                  1050  
 Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly  
                   1055                                  1060                                  1065  
 Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe  
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 <212> DNA  
 <213> Homo sapiens

B1  
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 ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200  
 cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250  
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<210> 104  
 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<400> 104

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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

B1

Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser
				380					385					390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly
				395					400					405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro
				410					415					420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly
				425					430					435
Leu	Tyr	Val	Gln	Met	Glu	Asn								
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<210> 105  
 <211> 21  
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<400> 105  
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<210> 106  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 106  
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<210> 107  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 107  
 agtcgcaggc agcgttgg 18

<210> 108  
 <211> 25  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 109  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

B1  
<400> 110  
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tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150  
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200  
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 aaaaaaaaaa gaaa 1114

<210> 111  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
 1 5 10 15  
 Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
 20 25 30  
 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
 35 40 45  
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
 50 55 60  
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
 65 70 75  
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
 80 85 90  
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
 95 100 105  
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
 110 115 120  
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
 125 130 135  
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
 140 145 150  
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
 155 160 165  
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
 170 175 180  
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
 185 190 195  
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

B1



	200		205		210
Arg Gly Phe Cys	Ser Ala Asp Ser Gly	Gly Pro Leu Val Cys	Arg		
	215		220		225
Asn Arg Ala His	Gly Leu Val Ser Phe	Ser Gly Leu Trp Cys	Gly		
	230		235		240
Asp Pro Lys Thr	Pro Asp Val Tyr Thr	Gln Val Ser Ala Phe	Val		
	245		250		255
Ala Trp Ile Trp	Asp Val Val Arg Arg	Ser Ser Pro Gln Pro	Gly		
	260		265		270
Pro Leu Pro Gly	Thr Thr Arg Pro Pro	Gly Glu Ala Ala			
	275		280		

<210> 112

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

cgagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

gagctacca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50

cctgacgcct gacgcctgtc cccggccccg catgagccgc tacctgctgc 100  
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
 tatgtcaccg gtggggcctt cccagcaag gccaccatcc ctgggaagac 200  
 ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250  
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
 aagtgtgagg cggcagcaaa ggacatccgc ggggagacc tcaatcacca 350  
 tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400  
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450  
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500  
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg aaaaacttgc 550  
 tgctggacaa gctgaaagcc tcagcccctt cgcgatcat caacctctcg 600  
 tccctggccc atgttgctgg gcacatagac ttgacgact tgaactggca 650  
 gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700  
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750  
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 cacgggcac ccatggctcca ctttctccag caccacactc gggcccatct 850  
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 ctggccgtgg cggaggaact ggcgatgtt tccgaaagt acttcgatgg 950  
 actcaaacag aaggccccg ccccgaggc tgaggatgag gaggtggccc 1000  
 ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050  
 gtgaggagc agcccctccc cagataacct ctggagcaga ttgaaagcc 1100  
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 agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350  
 ggaggaagg gctctgtgca cttgcaggcc acgtcaggag agccagcgg 1400  
 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450

B1

tctgacactt ggtggattct tgggtccctg tgggaccttg tgcattgcatg 1500  
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ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650  
gagagcaggt gcaggtgtca tcccagagttc aggctctgca cggcatggag 1700  
tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
gctcattt 1808

<210> 116  
<211> 331  
<212> PRT  
<213> Homo sapiens

<400> 116

Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
1 5 10 15  
Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
20 25 30  
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
35 40 45  
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
50 55 60  
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
65 70 75  
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
80 85 90  
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
95 100 105  
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
110 115 120  
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
125 130 135  
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
140 145 150  
Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
155 160 165  
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
170 175 180

B1

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	
				230					235					240	
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	
				245					250					255	
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	
				260					265					270	
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	
				275					280					285	
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	
				290					295					300	
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	
				305					310					315	
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	
				320					325					330	

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggtcgc 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgccccg 150  
 agcgccgggt gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200  
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccagagg tgtctttcag 500  
 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550  
 ttctctcaca ggggatgact gcttccaagt tggcaagggtg gcctatgaca 600  
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650  
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700  
 agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
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 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000  
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 tggagcccta cattgctctc taccatgact tcgtcagtga ctacagaggct 1100  
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
 ggctgaagga cactgttgac caaaaactgg tgaccctcaa ccaccgcatt 1250  
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450  
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500  
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550  
 gctggctgtc ctgtcctggg gggagataag tgggtggcca acaagtggat 1600  
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700  
 aagccaggag caaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800  
 gggagagggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850

B1



Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly  
 185 190 195  
 Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu  
 200 205 210  
 Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser  
 215 220 225  
 Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala  
 230 235 240  
 Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu  
 245 250 255  
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr  
 260 265 270  
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala  
 275 280 285  
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr  
 290 295 300  
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr  
 305 310 315  
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala  
 320 325 330  
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu  
 335 340 345  
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala  
 350 355 360  
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val  
 365 370 375  
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser  
 380 385 390  
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr  
 395 400 405  
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro  
 410 415 420  
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly  
 425 430 435  
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro  
 440 445 450  
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile  
 455 460 465

131

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys  
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser  
530 535 540

Ser Pro Glu Asp

B1  
<210> 119

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens



<400> 122

gagatagggga gtctggggttt aagttcctgc tccatctcag gagcccctgc 50  
tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcgggcc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200  
cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300  
ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctct 400  
gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550  
gaccattgac ttcctgaacg acaacattcg aagaggaatt gagaactact 600  
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
cgactgcagt gccctggac ccctggcctg tggggtgccc tacacctgct 750  
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
atcgacaagg agcgtttcag tgtgcaggat gtcacttacg tgcggggctg 850  
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950  
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tgatgggctc ctggggcccg gtgccaaagg cagcgtggag gcggcaggca 1050  
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agagcctggg cctcccctaa gaggctttcc ccgaggcagc tctggaatct 1300  
gtgcccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350  
ctacagggga gggagagcct gaggtctgc tcaggggcca tttcatctct 1400

B1

ggcagtgcct tggcgggtggt attcaaggca gttttgtagc acctgtaatt 1450  
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500  
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550  
 ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggctgct 1600  
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650  
 gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
 gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750  
 catgttttgt tttgttttta aaaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
 1 5 10 15

Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val  
 20 25 30

Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
 35 40 45

Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60

Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
 65 70 75

Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
 80 85 90

Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
 95 100 105

Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
 110 115 120

Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
 125 130 135

Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150

Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165

Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly

B1

	170	175	180
Val Pro Tyr Thr	Cys Cys Ile Arg Asn	Thr Thr Glu Val Val	Asn
	185	190	195
Thr Met Cys Gly	Tyr Lys Thr Ile Asp	Lys Glu Arg Phe Ser	Val
	200	205	210
Gln Asp Val Ile	Tyr Val Arg Gly Cys	Thr Asn Ala Val Ile	Ile
	215	220	225
Trp Phe Met Asp	Asn Tyr Thr Ile Met	Ala Cys Ile Leu Leu	Gly
	230	235	240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu	Tyr
	245	250	255
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr	Asp
	260	265	270
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala	Gly
	275	280	285
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn		
	290		

<210> 124

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 124

atcatctatt ccaccgtggt ctggc 25

<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gacagagtgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50

gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100

ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150

tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200

agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250

agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300

ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350

acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400

gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450

gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500

tggacaccag tgcaagtggc cccaccgcgc tggctcctcag tgactgtgcc 550

accagccatg ggagcctgcg catccaactg ctgtataagc tctccttctt 600

ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtgc ccatccctgc 650

ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700

ggcatgtatg cagacctcct gcagctgggtg aaggtgccc tttccctcag 750

cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800

ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg 850

accaagtggc tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900

caacatcccg ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950

tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000

cttcttgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050

aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100

aggacactcc cgagtttttt atagaccaag gccatgccc ggtggcccaa 1150

ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200

caccctgggc atcgaagcca gctcgggaagc tcagttttac accaaagggtg 1250

B1

accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
 atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
 cactgagatc atccactcca tctgtctgcc gaaccagaat ggcaaattaa 1400  
 gatctggggg cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450  
 gagtcctcac tgaccaagga tgcccttgtg cttactccag cctccttgtg 1500  
 gaaaccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550  
 ggaaggctgg gtccagctg ggagtatggg tgtgagctct atagaccatc 1600  
 cctctctgca atcaataaac acttgctgt gaaaaa 1636

<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

<400> 128

Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala  
 1 5 10 15

Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile  
 20 25 30

Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
 35 40 45

Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
 50 55 60

Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
 65 70 75

Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
 80 85 90

Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
 95 100 105

Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
 110 115 120

Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
 125 130 135

Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
 140 145 150

Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
 155 160 165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

170 175 180

Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
185 190 195

Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
200 205 210

Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys  
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser  
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu  
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser  
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu  
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His  
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp  
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr  
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu  
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu  
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr  
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp  
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp  
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu  
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu  
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys

B1

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
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Pro Val Ser Gln

<210> 129

<211> 2213

<212> DNA

<213> Homo sapiens

<400> 129

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aaagaaggag atggtgttat ctgaaaagggt tagtcagctg atggaatgga 150

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gtgaaagccc caccgagaaa ttactccggt atcgtcatgt tcaactgctct 250

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agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350

ttttttgcc tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400

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ccaaacgggg tgatacatat gagttacagg tgcgggggttt ttcagctgag 500

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ggaaattgaa aaacgaaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100

B1

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 aactactact ttgttttagt tagaacaag ctcaaaacta ctttagtta 1350  
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 aaaaaaaaaa aaa 2213

<210> 130  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
 Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val  
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Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln



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Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met	35	40	45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys	50	55	60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile	65	70	75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys	80	85	90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg	95	100	105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp	110	115	120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser	125	130	135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg	140	145	150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln	155	160	165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val	170	175	180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu	185	190	195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met	200	205	210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys	215	220	225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg	230	235	240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn	245	250	255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His	260	265	270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu	275	280	285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys	290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser			

B1

	305		310		315
Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr					
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Ser Phe Leu Met Ser					
	335				

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200  
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250  
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300  
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350  
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
 ttaacagaat cttggaataa ttttaaggtg ctagatccaa attatacaac 450  
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 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100

B1

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 gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350  
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 cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450  
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B/

<210> 132  
<211> 536  
<212> PRT  
<213> Homo sapiens

<400> 132

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Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys  
20 25 30  
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
35 40 45  
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
50 55 60  
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
65 70 75  
Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly  
80 85 90  
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu  
95 100 105  
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly  
110 115 120  
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His  
125 130 135  
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala  
140 145 150  
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg  
155 160 165  
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr  
170 175 180  
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr  
185 190 195  
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr  
200 205 210  
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His  
215 220 225  
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys  
230 235 240  
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr  
245 250 255

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys  
 260 265 270  
 Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu  
 275 280 285  
 Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu  
 290 295 300  
 Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly  
 305 310 315  
 Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr  
 320 325 330  
 Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile  
 335 340 345  
 Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile  
 350 355 360  
 Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn  
 365 370 375  
 Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys  
 380 385 390  
 Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser  
 395 400 405  
 Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg  
 410 415 420  
 Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile  
 425 430 435  
 Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr  
 440 445 450  
 Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln  
 455 460 465  
 Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val  
 470 475 480  
 His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile  
 485 490 495  
 Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln  
 500 505 510  
 Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln  
 515 520 525  
 Trp Leu Lys Thr His Met Asn Pro Arg Ala Val  
 530 535

B1

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133

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B1

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 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu  
 1 5 10 15  
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp  
 20 25 30  
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly  
 50 55 60  
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala  
 65 70 75  
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile  
 80 85 90  
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr  
 95 100 105  
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala  
 110 115 120  
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro  
 125 130 135  
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro  
 140 145 150  
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr  
 155 160 165  
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile  
 170 175 180  
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr  
 185 190 195  
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg  
 200 205 210

B1

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser  
 215 220 225

Leu Thr Gly Tyr Val  
 230

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 aagtcatcgc tcccgtggc tcagaaccat ggctgtgcca gccggcaccc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcca atgtgggtccc ccctgcacct 250  
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 gattttgttg tgaagctgaa ggttcagggg gtgaattccc agtgccactc 350  
 atctcccatc tccagtaaag gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
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 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys





Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met  
                   20                                  25                                  30  
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp  
                   35                                  40                                  45  
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val  
                   50                                  55                                  60  
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg  
                   65                                  70                                  75  
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu  
                   80                                  85                                  90  
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu  
                   95                                  100                                  105  
 Cys Arg Ser Val Ser  
                                   110

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
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 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
 atacccgagg ccaaagtcag gcacccccctg tcctatgtgg cccagcggca 950  
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 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450  
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 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750  
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 gttgccccac cactggaga tgggtgctgag ggaggtgggt ggggccttct 1850  
 gggaaggtga gtggagagg gcacctgcc cccgccctcc ccatcccta 1900  
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<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly  
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Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val  
20 25 30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
35 40 45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
50 55 60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
65 70 75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
80 85 90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
95 100 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
110 115 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
125 130 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu  
140 145 150

Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu  
155 160 165

Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val  
170 175 180

Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala  
185 190 195

Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu  
200 205 210

Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg  
215 220 225

Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile  
230 235 240

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro  
245 250 255

Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln  
260 265 270

Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro

B1

	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141

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 cttagacctc ctttctgcc ctcttttctt gcccaccgct gcttcttggc 150  
 ctttctccga ccccgctcta gcagcagacc tcctgggggc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccact 250  
 ccgctcccgg accagcggcc tgaccctggg gaaaggatgg ttcccagagt 300  
 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttcccctgg 350  
 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400  
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 gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
 accgcctcca ctgtccgct gtccactgcc cccagcctgt gacggagcca 550  
 cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
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 agatcttcag tgcccatgag ctgttccctt cccgcctgcc caaccagtgt 700  
 gtctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
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 tgggagaaaag agaggcccgg gcacccagc cccactggc ctcagcgccc 950  
 ctctgagctt catccctcgc cacttcagac ccaaggagc aggcagcaca 1000  
 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
 cggaagacg tactcccacg gggagggtgtg gcacccggcc ttccgtgcct 1100

B1

tcggccccctt gccctgcac cttatgcacct gtgaggatgg ccgccaggac 1150  
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 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
 ctctgccaca catcgggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
 cctggaacac gaggcctcgg acttgggtgga gatctacctc tggaagctgg 1400  
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
 ccacacagcc agaattcttc acttgactca gatcaagaaa gtcaggaagc 1500  
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggcccccac 1550  
 gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
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 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
 <211> 451  
 <212> PRT  
 <213> Homo sapiens

<400> 142  
 Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala  
 1 5 10 15  
 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp  
 20 25 30  
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser  
 35 40 45  
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg  
 50 55 60  
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His  
 65 70 75  
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln  
 80 85 90  
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg  
 95 100 105  
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His  
 110 115 120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro  
 125 130 135  
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys  
 140 145 150  
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro  
 155 160 165  
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu  
 170 175 180  
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg  
 185 190 195  
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly  
 200 205 210  
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe  
 215 220 225  
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val  
 230 235 240  
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly  
 245 250 255  
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg  
 260 265 270  
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly  
 275 280 285  
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys  
 290 295 300  
 Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro  
 305 310 315  
 Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg  
 320 325 330  
 Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser  
 335 340 345  
 Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala  
 350 355 360  
 Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu  
 365 370 375  
 Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His  
 380 385 390  
 Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala  
 395 400 405

131

Arg	Leu	Pro	Glu	Arg	Gly	Thr	Ala	Leu	Pro	Thr	Ala	Arg	Trp	Pro
				410					415					420
Pro	Arg	Arg	Ser	Leu	Glu	Arg	Leu	Pro	Ser	Pro	Asp	Pro	Gly	Ala
				425					430					435
Glu	Gly	His	Gly	Gln	Ser	Arg	Gln	Ser	Asp	Gln	Asp	Ile	Thr	Lys
				440					445					450

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
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 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
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 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgccg 400  
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450  
 ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500  
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30



Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
                             35                            40                            45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
                             50                            55                            60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
                             65                            70                            75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
                             80                            85                            90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 caggctgcc a tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
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 acaccatctc cgggagagtg gatcgtcttg agcgggaggt agactatctg 400  
 gagaccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450  
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 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600  
 gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650  
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 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
 aaccgaacag tgggtggacag ctcaagtatt ccagcagagg ggctgatccc 900

B1

cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
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 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<400> 146  
 Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp  
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 Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met  
 20 25 30  
 Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln  
 35 40 45  
 Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn

				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala
				260					265					270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala
				275					280					285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys
				290					295					300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro
				305					310					315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr
				320					325					330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile

B1

	335		340		345
Gln Cys Ser Phe	Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg	Ala		
	350	355	360		
Ala Leu Pro Tyr	Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser	Leu		
	365	370	375		
Arg Tyr Asn Pro	Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp	Gly		
	380	385	390		
Tyr Gln Ile Val	Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu	Glu		
	395	400	405		

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

B1

<400> 147  
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 gttctctct tctctctaatt ccatccgtca cctctcctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
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 gccagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctcct 300  
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 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggaggggagc atctctctga ggctggaaaa cattactgtg 500  
 ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
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 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850

aggagataacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
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 ttctttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050  
 tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100  
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250  
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
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 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
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 atagtcatct gcccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
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 cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac 1800  
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 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950  
 tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
 acagagtgta tcctaattgg ttgttcatta tattacactt tcagtaaaaa 2050  
 aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1	5	10	15
Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val	Gln Ala
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Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser	Pro Lys
	35	40	45
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly	Gln Phe
	50	55	60
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln	Pro Phe
	65	70	75
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val	Lys Asp
	80	85	90
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn	Ile Thr
	95	100	105
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser	Gln Ser
	110	115	120
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala	Leu Gly
	125	130	135
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg	Asp Ile
	140	145	150
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro	Thr Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp	Ser Arg
	170	175	180
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile	Ser Leu
	185	190	195
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met	Arg His
	200	205	210
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile	Gly Asp
	215	220	225
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys	Val Leu
	230	235	240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly	Leu Lys
	245	250	255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu	Leu Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala	Arg Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His	Pro Lys

B1

290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 151  
gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

B/

<400> 152  
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aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
gcctcgccct gttgtgtgc gccgccgccg ccgccgccgt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250  
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
gggcgacggc tcccacggcc caggccccga ggaccgggcc ccgcgcgcc 350  
accgtccacc gacccttggc tgcgacttct ccagcccagt ccccgagac 400  
caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500  
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ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150  
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B1

tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250

agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys  
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Ala Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn  
20 25 30

Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro  
35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala  
50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala  
65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro  
80 85 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr  
95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala  
110 115 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro  
125 130 135

Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val  
140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro  
155 160 165

Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro  
170 175 180

Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn  
185 190 195

Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr  
200 205 210

Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys  
215 220 225

Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu  
230 235 240

B1

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro  
245 250 255

Cys Asn Arg

<210> 154  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
aactgctctg tgggttgaag cctg 24

<210> 155  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155  
cagtcacatg gctgacagac ccac 24

B1  
<210> 156  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 156  
agggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
<211> 689  
<212> DNA  
<213> Homo sapiens

<400> 157  
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ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150  
ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200  
tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcc aatctttcac tcagctggag 400  
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgctccc cagtagggat ggcgccaca 600  
 gggtcctgtg acctcggcca gtgtccacc acctcgctca gcggtcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158

Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90  
 Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu  
 95 100 105  
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile  
 110 115 120  
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu  
 125 130 135  
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu  
 140 145 150  
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln  
 155 160

<210> 159

<211> 1665  
<212> DNA  
<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
gtccatgtgc cctgtctcct ctctacccc tcgcatggct ggatttacct 200
tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
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cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300
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cttctgccccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350  
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 caccgagtagc tcggagatca agatccacag atgagaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550  
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 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	
1				5					10					15	
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	
				20					25					30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	
				35					40					45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	
				50					55					60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	
				65					70					75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	
				80					85					90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	
				95					100					105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	
				110					115					120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	
				125					130					135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	
				140					145					150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	
				155					160					165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	
				170					175					180	

Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg	Ser
	185	190	195
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr	Ser
	200	205	210
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr	Asn
	215	220	225
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu	Thr
	230	235	240
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu	Gly
	245	250	255
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg	Leu
	260	265	270
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg	Leu
	275	280	285
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro	Ser
	290	295	300
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp	Ala
	305	310	315
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln	Gln
	320	325	330
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly	Val
	335	340	345
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val	Phe
	350	355	360
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg	Lys
	365	370	375
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile	Glu
	380	385	390
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu	Thr
	395	400	405
Glu Pro Trp Ala	Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro	Ala
	410	415	420
Ser Ala Arg Ser	Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala	Ser
	425	430	435
Leu Ser Phe Gln	Met Val Lys Pro Trp	Asp Ser Arg Gly Gln	Glu
	440	445	450
Ala Thr Asp Thr	Glu Tyr Ser Glu Ile	Lys Ile His Arg	
	455	460	

<210> 161  
<211> 739  
<212> DNA  
<213> Homo sapiens

<400> 161  
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gagggaggat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300  
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aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650  
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
<211> 170  
<212> PRT  
<213> Homo sapiens

<400> 162  
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1 5 10 15  
Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr  
20 25 30  
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg  
35 40 45  
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly  
50 55 60  
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile  
65 70 75



Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	
				80					85					90	
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	
				95					100					105	
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	
				110					115					120	
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	
				125					130					135	
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	
				140					145					150	
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	
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Cys	Val	Pro	Glu	His											
				170											

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 165  
 gtcctccgga aagtccttat c 21

<210> 166  
 <211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
gcctagtgtt cggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
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<210> 168  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 168  
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<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169  
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aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150  
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200  
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250  
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ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggagg 350  
ctgtgagcag acccgacag cactgagtc cttccccac ccggcttca 400  
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500

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cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
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ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcacctc catttccact 900
tggtgttttg ttcctgttca ctctgtta atagaaaccct aagccaagac 950
cctctacgaa cattcttttg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctgggtt tgttctctgt 1100
tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
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<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

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Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
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Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
              20              25              30

His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
              35              40              45

Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
              50              55              60

Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
              65              70              75

Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
              80              85              90

Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
              95              100             105

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Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
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<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcgga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 173  
cctctgggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
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<220>  
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<400> 175  
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<210> 176  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 176  
cccttgatga tcctggtc 18

<210> 177  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 177  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 178  
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179  
<211> 907  
<212> DNA  
<213> Homo sapiens

<400> 179  
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aagaaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150  
agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200  
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250  
caaaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300  
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350  
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400  
ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
tgtgaccaa ggaccacgga gcattgagac atttaaacia atagacatgg 500  
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750  
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ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
aaaaaaa 907

<210> 180  
<211> 222  
<212> PRT  
<213> Homo sapiens

<400> 180  
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Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				215	220	

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 182  
gacatggaca atgacagg 18

<210> 183  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 183  
cctttcagga tgtaggag 18

<210> 184  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 184  
gatgtctgcc accccaag 18

<210> 185  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcacccctgat atgacttgtc acgtggc 27

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
tacaagaggg aagaggagtt gcac 24

<210> 187  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Synthetic oligonucleotide probe

<400> 187

gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgtccc 100

cccaaagtct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150

atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

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ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

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Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
65 70

<210> 190  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 190  
agggaccatt gcttcttcca ggcc 24

<210> 191  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
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ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
gactttggaa gtgaccacc atggggctca gcatcttttt gtcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cgggggtgtc cttattgacc acagggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgcttggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500  
 gccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
 gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
 cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700  
 atgcctgcc a ggggtgattct gggggccccc tgggtgtgtgg gggagtcctt 750  
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800  
 ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000  
 gccagccctt ctaagacca cgagcggggg gagagaagtg tgcaatagtc 1050  
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr
				125					130					135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His
				140					145					150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser
				155					160					165
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile
				170					175					180
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala
				185					190					195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu
				200					205					210
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp
				215					220					225
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp
				230					235					240
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn							
				245										

<210> 195

<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

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tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
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caagaccacac ctggagatga agaagatgat ctgagagggt acaggagggg 400
tcagtgcacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600

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ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650  
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 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
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 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 196  
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 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn  
                   20                  25                  30  
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu  
                   35                  40                  45  
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
                   50                  55                  60  
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met  
                   65                  70                  75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys	80	85	90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr	95	100	105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu	110	115	120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro	125	130	135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro	140	145	150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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ggggtcggcg ccgccgtgcg cgcccgcctg gcgctggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
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tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
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acaacaacat cagtcgcatc ctggtcacca gcttcaacca catgccgaag 700
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cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggatgtg 850
cagaagaagg agtacgtgtg cccagcccc cactcggagc cccatcctg 900

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caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950  
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tgaggagacc ttcacccagt acaagaaact gaagcgaata gacatcagca 1100  
agaatcagat atcggatatt gctccagatg ccttcagggg cctgaaatca 1150  
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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				20					25					30

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

	35	40	45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro	50	55	60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg	65	70	75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu	80	85	90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe	95	100	105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys	110	115	120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu	125	130	135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg	140	145	150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp	155	160	165
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr			

				320						325					330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	
				335					340					345	
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	
				350					355					360	
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	
				365					370					375	
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	
				380					385					390	
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	
				395					400					405	
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	
				410					415					420	
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	
				425					430					435	
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	
				440					445					450	
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser	
				455					460					465	
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser	
				470					475					480	
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe	
				485					490					495	
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg	
				500					505					510	
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg	
				515					520					525	
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn	
				530					535					540	
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys	
				545					550					555	
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys	
				560					565					570	
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu	
				575					580					585	
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val	
				590					595					600	
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn	

	605	610	615
Leu Ile Ser Cys	Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser	Ser
	620	625	630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile	Thr
	635	640	645
Pro Gly Ala Phe	Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn	Leu
	650	655	660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys	His Leu Ala Trp Leu	Gly
	665	670	675
Lys Trp Leu Arg	Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg	Cys
	680	685	690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val	Ala
	695	700	705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys	Gln
	710	715	720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr	Val
	725	730	735
Val Arg Cys Ser	Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly	Met
	740	745	750
Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu	Thr
	755	760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu	Ile
	770	775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr	Phe
	785	790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn	Arg
	800	805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser	Leu
	815	820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro	Glu
	830	835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu	Gly
	845	850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser	Glu
	860	865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys	Ser
	875	880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro	Thr

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala		
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr		
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr		
935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile		
950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser		
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly		
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys		
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys		
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile		
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys		
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Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
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Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
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<220>  
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<400> 199  
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<210> 200  
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<400> 200  
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<210> 201  
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 <211> 148  
 <212> PRT  
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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
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 35 40 45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
 50 55 60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
 65 70 75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
 80 85 90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
 95 100 105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
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Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
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Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
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<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

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<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctgggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

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<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

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<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

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<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

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				20					25					30

Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His
				35					40					45

Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg
				50					55					60

Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly
				65					70					75

Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val
				80					85					90

Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val
				95					100					105

Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro
				110					115					120

Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu
				125					130					135

Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala
				140					145					150

Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	155		160		165
Trp Glu Arg Val	His Leu Ile Val Ala	Gly Gly Tyr Asp Glu Arg			
	170	175			180
Val Leu Glu Asn	Val Glu His Tyr Gln	Glu Leu Lys Lys Met Val			
	185	190			195
Gln Gln Ser Asp	Leu Gly Gln Tyr Val	Thr Phe Leu Arg Ser Phe			
	200	205			210
Ser Asp Lys Gln	Lys Ile Ser Leu Leu	His Ser Cys Thr Cys Val			
	215	220			225
Leu Tyr Thr Pro	Ser Asn Glu His Phe	Gly Ile Val Pro Leu Glu			
	230	235			240
Ala Met Tyr Met	Gln Cys Pro Val Ile	Ala Val Asn Ser Gly Gly			
	245	250			255
Pro Leu Glu Ser	Ile Asp His Ser Val	Thr Gly Phe Leu Cys Glu			
	260	265			270
Pro Asp Pro Val	His Phe Ser Glu Ala	Ile Glu Lys Phe Ile Arg			
	275	280			285
Glu Pro Ser Leu	Lys Ala Thr Met Gly	Leu Ala Gly Arg Ala Arg			
	290	295			300
Val Lys Glu Lys	Phe Ser Pro Glu Ala	Phe Thr Glu Gln Leu Tyr			
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Arg Tyr Val Thr	Lys Leu Leu Val				
	320				

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
tttgcatagag ttcttggtta atttgcata gagatatggg cctgtggtct 250
ccttctggtt tggcaggcgc ctcgttggtta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400

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accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
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 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
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<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala		20	25	30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu		35	40	45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn		50	55	60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg		65	70	75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His		80	85	90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys		95	100	105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn		110	115	120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu		125	130	135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu		140	145	150
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser		155	160	165
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val		170	175	180
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln		185	190	195
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu		200	205	210
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu		215	220	225
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys		230	235	240
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser		245	250	255
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser		260	265	270
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys		275	280	285
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys		290	295	300

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305						310				315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320						325				330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335						340				345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350						355				360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365						370				375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380						385				390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395						400				405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410						415				420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425						430				435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440						445				450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455						460					

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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tcagggcttg tgccctctcg cttcctgacg ctctggcgc atctggtggt 150
cgatcatcacc ttattctggt cccgggacag caacatacag gctgcctgc 200
ctctcacgtt caccoccgag gagtatgaca agcaggacat tcagctggtg 250
gccgcgtct ctgtaccct gggcctcttt gcagtggagc tggccggttt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcaccc gtggccctgt cttcttcat attcgagcgt 400
tgggagtgc ctacgtattg gtacatTTTT gtcttctgca gtgcccttcc 450

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agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600  
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
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aaaaaaaa 759

<210> 214  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 214  
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Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
20 25 30  
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
35 40 45  
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
50 55 60  
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
65 70 75  
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
80 85 90  
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
95 100 105  
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
110 115 120  
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
125 130 135  
Lys Lys Lys Pro Phe  
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<210> 215  
<211> 697  
<212> DNA  
<213> Homo sapiens

<400> 215  
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ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgacctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggcttact ggctgcggg gtggctcagg 500
gagccctgag gtccaactat gtgtcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcattccaga attggccaca 600
ctaccgctcc cctgagggcc ctgctgatcc gcacccatt cctcccctcc 650
catggcctaaa aacccactg tctccttctc caataaagat gtagctc 697

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<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	1	5	10	15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	20	25	30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	35	40	45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	50	55	60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	65	70	75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	80	85	90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	95	100	105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	110	115	120	

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200
gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250
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ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
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gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
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gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850

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ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900  
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 gccagggcca agtctcaagt ggcagagaaa ggggtcccaag tgctgggtccc 1000  
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050  
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 aataaagctt gccccgggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

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Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20					25					30
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	215	220	225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	230	235	240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				245	250	

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200

gcgcccgcgc cgccgtcgct cctgcagcgc tgtcgacctc gccgctagca 250  
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agcgccagcc ggctgcggtc gccacacgg ctcaccatgg gctccgggcg 350  
ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400  
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gaattttatt tgtttagttt taaaagactg gcaaccagggt ctaaggatta 1300  
gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgcca 1350  
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400  
ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450  
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ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

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<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp	35	40	45	
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu	50	55	60	
Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	65	70	75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	80	85	90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	95	100	105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	110	115	120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	125	130	135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	140	145	150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	155	160	165	

Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu
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Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly
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 <223> Synthetic oligonucleotide probe

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 <212> DNA  
 <213> Artificial Sequence

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 <211> 40  
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 <213> Artificial Sequence

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 <211> 902  
 <212> DNA  
 <213> Homo sapiens

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<210> 225

<211> 257

<212> PRT

<213> Homo sapiens

<400> 225

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				20					25					30
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35					40					45
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile
				50					55					60
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
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Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80					85					90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
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Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
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Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
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Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
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Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
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Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
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Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
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Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
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 <211> 3939  
 <212> DNA  
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<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser
				35					40					45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn
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Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln
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Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val
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Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg
				95					100					105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro
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Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser

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Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg
				140					145					150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn
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<211> 2848

<212> DNA

<213> Homo sapiens

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<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
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Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
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Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
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Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
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Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
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Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
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Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
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Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu
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Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val		
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Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr		
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Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val		
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<223> Synthetic oligonucleotide probe

<400> 230

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<223> Synthetic oligonucleotide probe

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<211> 2786

<212> DNA

<213> Homo sapiens

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 <211> 421  
 <212> PRT  
 <213> Homo sapiens

<400> 234

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Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
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Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180	
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Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
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Tyr

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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950  
ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000  
ctcctacaat ctggaaacca tcctccgaa gatgggcac caaatgcct 1050  
ttgacaaaaa tgctgatttt tctggaattg caaagagaga ctccctgcag 1100  
gtttctaaag caaccacaa ggctgtgctg gatgtcagtg aagagggcac 1150  
tgaggccaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200  
gtccctctta cttcactgtc tccttcaata ggaccttct gatgatgatt 1250  
acaaataaag ccacagacgg tattctcttt ctagggaaag tggaaaatcc 1300  
cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350  
tgcacaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400  
tgacccagtg ggagctggat tcgctggcag ggatgccact tccaaggctc 1450  
aatcaccaaa ccatcaacag ggacccagtc cacaagccaa caccattaa 1500

cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcacg 1550  
 ggatgttgct gggttacat atttcattc cttggggctc ccaggaatgg 1600  
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac 1650  
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys  
 1 5 10 15  
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr  
 20 25 30  
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
 35 40 45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
 50 55 60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
 65 70 75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
 80 85 90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
 95 100 105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
 110 115 120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
 125 130 135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
 140 145 150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
 155 160 165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
 170 175 180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
 185 190 195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala  
 200 205 210

Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100

gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgccct cttaaagtctt ggtacatcta 200

ggaccagggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300  
aacaaattcc aatgagacta gcacctctgc caaactgga tccagtgtga 350  
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400  
agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450  
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500  
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550  
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600  
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650  
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tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag 750  
cacactctcc agtggggcca gcacagccac caactctgac tccagcaca 800  
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gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000  
gccaccaact ctgagtccag cagcacctcc agtggggcca gcacagccac 1050  
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100  
ctgagtccag cagcacctcc agtggggcca gcacagccac caactctgag 1150  
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200  
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250  
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agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350  
ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400  
gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450  
gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500  
caactctgac tccagcaca cctccagtga ggccagcaca gccaccaact 1550  
ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag 1600  
tccagcaca cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650  
tgtgacctct gcaggctctg gaacagcagc tctgactgga atgcacaca 1700

cttcccatag tgcattctact gcagtgcgtg aggcaaagcc tgggtgggtcc 1750  
 ctgggtgccgt gggaaatctt cctcatcacc ctggtctcgg ttgtggcggc 1800  
 cgtgggggtc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850  
 tgagaaacac cttaacaca gctgtctacc accctcatgg cctcaaccat 1900  
 ggccttggtc caggccctgg agggaaatcat ggagcccccc acaggcccag 1950  
 gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000  
 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050  
 gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt 2100  
 cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150  
 tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200  
 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250  
 acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300  
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350  
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243  
 <211> 596  
 <212> PRT  
 <213> Homo sapiens

<400> 243  
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu  
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 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser  
 20 25 30  
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala  
 35 40 45  
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala  
 50 55 60  
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val  
 65 70 75  
 Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala  
 80 85 90  
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala  
 95 100 105

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	365	370	375
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	380	385	390

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala	395	400	405
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	410	415	420
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Glu	Ala	Ser	Thr	Ala	425	430	435
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	440	445	450
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	455	460	465
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ala	Gly	Ser	Gly	Thr	Ala	470	475	480
Ala	Leu	Thr	Gly	Met	His	Thr	Thr	Ser	His	Ser	Ala	Ser	Thr	Ala	485	490	495
Val	Ser	Glu	Ala	Lys	Pro	Gly	Gly	Ser	Leu	Val	Pro	Trp	Glu	Ile	500	505	510
Phe	Leu	Ile	Thr	Leu	Val	Ser	Val	Val	Ala	Ala	Val	Gly	Leu	Phe	515	520	525
Ala	Gly	Leu	Phe	Phe	Cys	Val	Arg	Asn	Ser	Leu	Ser	Leu	Arg	Asn	530	535	540
Thr	Phe	Asn	Thr	Ala	Val	Tyr	His	Pro	His	Gly	Leu	Asn	His	Gly	545	550	555
Leu	Gly	Pro	Gly	Pro	Gly	Gly	Asn	His	Gly	Ala	Pro	His	Arg	Pro	560	565	570
Arg	Trp	Ser	Pro	Asn	Trp	Phe	Trp	Arg	Arg	Pro	Val	Ser	Ser	Ile	575	580	585
Ala	Met	Glu	Met	Ser	Gly	Arg	Asn	Ser	Gly	Pro					590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50  
ttccccgacct tcccagcaat atgcatcttg cacgtctggc cggctcctgc 100  
tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150  
ccccattgag aaggtcattg aagggatcaa ccgagggtg agcaatgcag 200  
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
tggaacaagg tgcccatgag atcaaccatg gtattggaca agcaggaaag 400  
gaagcagaga agcttggcca tgggggtcaac aacgtgtgtg gacaggccgg 450  
gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500  
ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgtgtgac 550  
cagggtggaa aggaagtggg gaagcttggc caaggtgccc accatgtgtg 600  
tgggcaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
ccagcaagga ggccaaccag ctgtgtaatg gcaaccatca aagcggatct 700  
tccagccatc aaggaggggc cacaaccacg ccgtagcct ctggggcctc 750  
agtcaacacg cctttcatca accttccgc cctgtggagg agcgtcgcca 800

acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
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 tttctgaaat ccctgaaggg ggttgactg ggatttga ataaacttga 950  
 tacacca 957

<210> 248  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 248  
 Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu  
 1 5 10 15  
 Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu  
 20 25 30  
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg  
 35 40 45  
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His  
 50 55 60  
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met  
 65 70 75  
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu  
 80 85 90  
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile  
 95 100 105  
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn  
 110 115 120  
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln  
 125 130 135  
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys  
 140 145 150  
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu  
 155 160 165  
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala  
 170 175 180  
 Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
 185 190 195  
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
 200 205 210  
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly

	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240
Ser Val Ala Asn Ile Met Pro			
	245		

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 250  
 aagcttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 251  
 tgacccatt gagaaggtca ttgaaggat caaccgagg ctg 43

<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens

<400> 252  
 ctccgggtcc ccaggggctg cgccggggccg gcctggcaag ggggacgagt 50  
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 tgaccctgac tcaactccagg tccggaggcg ggggcccccg gggcgactcg 150  
 ggggcggacc gcggggcgga gctgccgcc gtgagtccg ccgagccacc 200  
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ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300  
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 cccgggaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg 1500  
 aacttctca aggaccactt cctgatggac gggcaggctc gaagccgcat 1550  
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cgcccgggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900  
gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950  
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ttttgtacca acaggggaga agccatgtga gcaagtccag ttccagccca 2050  
acacagtga cactttggcc tgcccgtcc tctccaacct ggcgaccga 2100  
ctctggctac gcaacggggc ccccgtaat gcctcggcct cctgccacgt 2150  
gctaccact ggggacctgc tgctgggtgg caccacacag ctgggggagt 2200  
tccagtgtg gtcactagag gagggcttc agcagctgg agccagctac 2250  
tgcccagagg tgggtggagga cggggtggca gaccaaacag atgaggggtg 2300  
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ctaccggcac cggaacagca tgaaagtctt cctgaagcag ggggaatgtg 2500  
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ccagtccctg tcagacagcc ccccgggggc ccgagtcttc actgagtcag 2650  
agaagaggcc actcagcatc caagacagct tcgtggaggt atccccagtg 2700  
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
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Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
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Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile	
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Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly	
				140					145					150	
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn	
				155					160					165	
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp	
				170					175					180	
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala	
				185					190					195	
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe	
				200					205					210	
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro	
				215					220					225	
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe	
				230					235					240	
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	
				245					250					255	
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	
				260					265					270	
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	
				275					280					285	
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	
				290					295					300	
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	
				305					310					315	
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	
				320					325					330	
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	
				335					340					345	
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	
				350					355					360	
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys	
				365					370					375	
Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro	
				380					385					390	
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	
				395					400					405	

Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
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Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val
	665	670	675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro
	680	685	690



Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
				695					700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
				710					715					720	
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
				725					730					735	
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
				740					745					750	
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
				755					760					765	
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
				770					775					780	
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
				785					790					795	
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
				800					805					810	
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
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<210> 254

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 254

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<210> 255

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

tgaagccagg gcagcgtcct ctgg 24

<210> 256

<211> 18

<212> DNA

<213> Artificial Sequence

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<400> 256  
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<213> Homo sapiens

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<223> unknown base

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agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150  
  
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cgcccagagcc gccgctagcg cgcccggggc atggtccctt cttaaaggcg 250  
  
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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				20					25					30
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
				35					40					45
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val
				245					250					255
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser
				260					265					270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys

	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln	Ala
	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg	Leu
	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His	Arg
	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr	Ser
	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro	Pro
	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu	Glu
	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp	Gly
	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala	Leu
	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn	Ala
	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr	Gly
	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu	Asp
	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr	Val
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Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys	Ile
	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala	Lys
	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn	Ser
	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser	Glu
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His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro	Leu
	530	535	540
Ser Gly Arg Phe	Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu
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Lys Thr Cys Leu	Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu

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Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
				590					595					600					
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
				605					610					615					
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys					
				620					625					630					
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg					
				635					640					645					
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe					
				650					655					660					
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
				665					670					675					
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn					
				680					685					690					
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
				695					700					705					
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
				710					715					720					
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
				725					730					735					
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
				740					745					750					
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
				755					760					765					
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
				770					775					780					
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
				785					790					795					
Asn	Gly	Ser	Val	Arg	Thr	Ala													
				800															

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 261  
gtgccactac ggggtgtgga cgac 24

<210> 262  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 262  
tcccatttct tccgtggtgc ccag 24

<210> 263  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 263  
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<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
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gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250  
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300  
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350  
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400  
tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
gcttcacacc ggaaatagga aagaaaaaac acacggaaag tacccttcc 500  
tggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550  
ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaac 600  
aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650

ccatatgtta cctcatacaa gtcacctgtc accacttttag ataagagcac 700  
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750  
 aaactgcat agaaaaaccc gaagagtttg gaaagcacc agagagttgg 800  
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgca 850  
 acaggcactt cttagtgaca ccagcaaccc agcatataga gaagatattg 900  
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950  
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000  
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050  
 attctagatc taaactctat gaatatattg atattaaatg tgttcacca 1100  
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 tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200  
 aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250  
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300  
 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350  
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 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90

Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly	95	100	105
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro	110	115	120
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala	125	130	135
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	140	145	150
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val	155	160	165
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro	170	175	180
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu	185	190	195
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys	200	205	210
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp	215	220	225
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala	230	235	240
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu	245	250	255
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala	260	265	270
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro	275	280	285
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile	290	295	300
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp	305	310	315
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val	320	325	330
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala	335	340	345
Leu	Leu	Lys	Val	Tyr											350		

<210> 266  
 <211> 2403  
 <212> DNA

<213> Homo sapiens

<400> 266

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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150  
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcactg 200  
gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250  
tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt 300  
caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact 350  
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 tcccatattc atatgtccag tgtctgggg atgagacaga gaagaccctg 1550  
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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
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Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20				25					30	

Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35	40	45
Thr Ser Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Asn Gln	Phe
	50	55	60
His Ala Val Val	His Leu Tyr Arg Asp	Gly Glu Asp Trp Glu	Ser
	65	70	75
Lys Gln Met Pro	Gln Tyr Arg Gly Arg	Thr Glu Phe Val Lys	Asp
	80	85	90
Ser Ile Ala Gly	Gly Arg Val Ser Leu	Arg Leu Lys Asn Ile	Thr
	95	100	105
Pro Ser Asp Ile	Gly Leu Tyr Gly Cys	Trp Phe Ser Ser Gln	Ile
	110	115	120
Tyr Asp Glu Glu	Ala Thr Trp Glu Leu	Arg Val Ala Ala Leu	Gly
	125	130	135
Ser Leu Pro Leu	Ile Ser Ile Val Gly	Tyr Val Asp Gly Gly	Ile
	140	145	150
Gln Leu Leu Cys	Leu Ser Ser Gly Trp	Phe Pro Gln Pro Thr	Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Ser Asp Ser	Arg
	170	175	180
Ala Asn Ala Asp	Gly Tyr Ser Leu Tyr	Asp Val Glu Ile Ser	Ile
	185	190	195
Ile Val Gln Glu	Asn Ala Gly Ser Ile	Leu Cys Ser Ile His	Leu
	200	205	210
Ala Glu Gln Ser	His Glu Val Glu Ser	Lys Val Leu Ile Gly	Glu
	215	220	225
Thr Phe Phe Gln	Pro Ser Pro Trp Arg	Leu Ala Ser Ile Leu	Leu
	230	235	240
Gly Leu Leu Cys	Gly Ala Leu Cys Gly	Val Val Met Gly Met	Ile
	245	250	255
Ile Val Phe Phe	Lys Ser Lys Gly Lys	Ile Gln Ala Glu Leu	Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys
	290	295	300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala	Pro
	305	310	315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser	Val

	320		325		330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val					
	335		340		345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp					
	350		355		360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn					
	365		370		375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr					
	380		385		390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr					
	395		400		405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe					
	410		415		420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys					
	425		430		435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr					
	440		445		450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp					
	455		460		465

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 gtcattcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150  
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
 attttataaa tctccattaa gggaagaatt tgtcaagtct cagggttatca 350  
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
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aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100  
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ggaggaccac tggttagttc agatgctaga gatattctggg accttgctgg 1200  
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtgtt 1250  
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cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650  
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aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900



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caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050  
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cca 2103

<210> 269  
<211> 423  
<212> PRT  
<213> Homo sapiens

<400> 269  
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Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
35 40 45  
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
50 55 60  
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
65 70 75  
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
80 85 90  
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
95 100 105  
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
110 115 120  
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
125 130 135  
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
140 145 150  
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
155 160 165  
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
170 175 180  
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
185 190 195  
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
200 205 210

Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
				215					220					225	
Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	
				230					235					240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	
				245					250					255	
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	
				260					265					270	
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	
				275					280					285	
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	
				290					295					300	
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	
				305					310					315	
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	
				320					325					330	
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	
				335					340					345	
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	
				350					355					360	
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	
				365					370					375	
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	
				380					385					390	
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	
				395					400					405	
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	
				410					415					420	

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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			20					25					30	
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40					45	

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys		50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly		65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu		80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys		95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp		110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val		125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val		140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro		155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe		170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu		185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser		200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly		215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu				230	235	

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
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Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
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Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	
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Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	
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Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	
				170					175					180	
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
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Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
				215					220					225	
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
				230					235					240	
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
				245					250					255	
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
				275					280					285	
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
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<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	
				185					190					195	
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	
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Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	
				215					220					225	
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	
				230					235					240	
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	
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Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	
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Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	
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Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	
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Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	
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Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	
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Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	
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Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	
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 <213> Homo sapiens

<400> 276

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gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350  
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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

Gly Thr Met Asn	Asn Phe Leu Gly Ser	Glu Pro Ile Leu Met	Arg
200		205	210
Thr Leu Gly Ser	Gln Pro Val Leu Lys	Thr Asp Asn Phe Leu	Arg
215		220	225
Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser	Thr
230		235	240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe	Asp
245		250	255
Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys	Lys
260		265	270
Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr	Thr
275		280	285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu	Pro
290		295	300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser	Pro
305		310	315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln	Val
320		325	330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu	Asp
335		340	345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys	Glu
350		355	360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro	Arg
365		370	375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu	Thr
380		385	390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly	Thr
395		400	405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala	Val
410		415	420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met	Tyr
425		430	435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser	Gly
440		445	450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro	Asp
455		460	465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly	Ala
470		475	480

Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala	
				485					490					495	
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg	
				500					505					510	
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu	
				515					520					525	
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg	
				530					535					540	
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser	
				545					550					555	
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala	
				560					565					570	
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala	
				575					580					585	
Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	
				590					595					600	
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	
				605					610					615	
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	
				620					625					630	
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	
				635					640					645	
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	
				650					655					660	
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	
				665					670					675	
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	
				680					685					690	
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	
				695					700					705	
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	
				710					715					720	
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	
				725					730					735	
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	
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<210> 278  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 278  
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<210> 279  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 279  
gtctggtcct ggctgtccac ccag 24

<210> 280  
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<212> DNA  
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<210> 281  
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<212> DNA  
<213> Homo sapiens

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ttccttctcc ctggggtcct gctctcagag gctgccaaaa tcctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacggtcac aatgtcacca tgcttaacca caaaagaggt 250  
ccttttatgc cagattttta aaaggaagaa aatcatatc aagttatcag 300  
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450



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<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30

Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45

Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60

Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75

Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90

Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105

Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120

Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135

Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150

Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
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				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly
				260					265					270
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn
				275					280					285
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu
				290					295					300
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu
				305					310					315
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
				320					325					330
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
				335					340					345
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
				350					355					360
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
				365					370					375
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
				380					385					390
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
				395					400					405
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
				410					415					420
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser

	440		445		450
Pro Thr Gln Arg	Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr			
	455		460		465
Gly Gly Ala Thr	His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp			
	470		475		480
His Glu Gln Tyr	Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu			
	485		490		495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala			
	500		505		510
Val Trp Trp Leu	Arg Gly Ala Arg Lys	Val Lys Glu Thr			
	515		520		

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 283  
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<210> 284  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 284  
 tcaggctggt ctccaaagag aggg 24

<210> 285  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 285  
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286  
 <211> 2340  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
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ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100  
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gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290  
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<210> 291  
<211> 1570  
<212> DNA  
<213> Homo sapiens

<400> 291  
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ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150  
ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200  
ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250  
agccagcgct ctacaggagg acctgcgctg tcgcgcgagg ggtctgggag 300  
atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350  
tcacctggct caatagggtcc aagggtgaaa agcagctaca ggtcatctca 400  
gtgctccagt gggtcctgtc cttccttgta ctgggagtgg cctgcagtgc 450  
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acttcacttg gctggtgttt gactggaaca cacccaagaa aggtggcagg 550  
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<210> 292

<211> 388

<212> PRT

<213> Homo sapiens

<400> 292

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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	

Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	
				185					190					195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	
				200					205					210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	
				215					220					225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	
				230					235					240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	
				245					250					255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly	
				260					265					270	
Ala	Asp	Leu	Val	Pro	Ile	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr	
				275					280					285	
Lys	Gln	Val	Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Gln	
				290					295					300	
Lys	Lys	Phe	Gln	Lys	Tyr	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His	
				305					310					315	
Gly	Arg	Gly	Leu	Phe	Ser	Ser	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr	
				320					325					330	
Ser	Lys	Pro	Ile	Thr	Thr	Val	Val	Gly	Glu	Pro	Ile	Thr	Ile	Pro	
				335					340					345	
Lys	Leu	Glu	His	Pro	Thr	Gln	Gln	Asp	Ile	Asp	Leu	Tyr	His	Thr	
				350					355					360	
Met	Tyr	Met	Glu	Ala	Leu	Val	Lys	Leu	Phe	Asp	Lys	His	Lys	Thr	
				365					370					375	
Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val	Leu	Glu	Val	Asn			
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<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

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<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

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ccgacgcagg gccggggccg gcccagggcc gaggagcgcg gcggccagag 100

cggggcccg cgaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150

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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
			20						25					30

Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
			35						40					45

Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
			50						55					60

Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
			65						70					75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
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Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln												

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 298  
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<210> 299  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 299  
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<210> 300  
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 <212> DNA  
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<400> 300  
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<210> 301  
 <211> 1334  
 <212> DNA  
 <213> Homo sapiens

<400> 301  
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 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



				65					70					75	
Gly	Leu	Arg	Pro	Ala 80	Ser	Ser	Val	Lys	Phe 85	Leu	Gly	Ser	Ala	Tyr 90	
Thr	Phe	Phe	Ser	Leu 95	Thr	Trp	His	Thr	Leu 100	Leu	Lys	Ala	Ser	Gln 105	
Gly	Phe	Ser	Leu	Phe 110	Leu	Gly	Ser	Lys	Tyr 115	Leu	Glu	Leu	Gln	Glu 120	
Pro	Ser	Trp	Ser	Gly 125	Pro	Cys	Pro	Pro	Gly 130	Gln	Leu	His	Cys	Thr 135	
Cys	Gly	Val	Leu	Leu 140	Ser	Phe	Leu								

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<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

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				20					25					30
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro

				65						70					75
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala	
				80					85					90	
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 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

<400> 306

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Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys	35	40	45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser	50	55	60	
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105	
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Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240	
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Leu Thr Leu Ala Phe Lys Ile  
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<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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				20					25					30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

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Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro	50		55		60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys	65		70		75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala	80		85		90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala	95		100		105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp	110		115		120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala	125		130		135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser	140		145		150
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser	155		160		165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala	170		175		180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu	185		190		195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala	200		205		210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys	215		220		225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser	230		235		240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser	245		250		255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val	260		265		270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro	275		280		285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser	290		295		300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu	305		310		315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg					

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Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg					
				365					370					375					
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly					
				380					385					390					
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu					
				395					400					405					
Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser					
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Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg					
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Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr					
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Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys					
				455					460					465					
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser					
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Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg					
				485					490					495					
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser					
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Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys					
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Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala					
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Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys					
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Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala					
				575					580					585					
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala					
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Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu					



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Asp Lys Glu His	Glu Glu Gly Arg Asp	Ser Glu Glu Gly Pro	Arg		
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Cys Gly Ser Ser	Glu Asp Leu His Asp	Ser Val Arg Glu Gly Pro			
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Asp Leu Asp Arg	Pro Gly Ser Asp Arg	Gln Glu Arg Glu Arg Ala			
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 <212> DNA  
 <213> Homo sapiens

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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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				20					25					30

Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
				50					55					60

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75

Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile
				80					85					90

Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105

Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
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Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135

Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150

Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165

Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170					175					180

Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195

Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210

Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225

His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly

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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro
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Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu
				260					265					270
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
				275					280					285
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
				290					295					300
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser
				305					310					315
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu
				320					325					330
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
				335					340					345
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
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Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His
				365					370					375
Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile
				380					385					390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro
				395					400					405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe
				410					415					420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala
				425					430					435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr
				440					445					450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp
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Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val
				470					475					480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu
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Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu
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Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala
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Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr
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Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu
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Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu
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Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu
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Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp
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His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp
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Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg  
 50 55 60  
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu  
 65 70 75  
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala  
 80 85 90  
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser  
 95 100 105  
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp  
 110 115 120  
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu  
 125 130 135  
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro  
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Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
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Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
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Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	
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Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	
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Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
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Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
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Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	
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Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	
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Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	
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Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	
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<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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cctcccaaag tgctgggatt acagggtgtga gccaccacgc ccggtacata 4150  
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atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250  
ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300  
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aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg	
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				20					25					30	
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
				35					40					45	
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	
				50					55					60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	
				65					70					75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	
				80					85					90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	
				95					100					105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	
				110					115					120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	
				125					130					135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu	
				140					145					150	
Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu	
				155					160					165	
Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile	
				170					175					180	
Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn	
				185					190					195	
Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala	
				200					205					210	
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val	
				215					220					225	
Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg	
				230					235					240	
Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His	

245				250				255						
Pro	Ser	Ile	Arg	Asn	Pro	Val	Ser	Leu	Val	Val	Thr	Arg	Leu	Val
				260					265				270	
Ile	Leu	Gly	Ser	Gly	Glu	Glu	Gly	Pro	Gln	Val	Gly	Pro	Ser	Ala
				275					280					285
Ala	Gln	Thr	Leu	Arg	Ser	Phe	Cys	Ala	Trp	Gln	Arg	Gly	Leu	Asn
				290					295					300
Thr	Pro	Glu	Asp	Ser	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu
				305					310					315
Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	Leu
				320					325					330
Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys
				335					340					345
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala
				350					355					360
His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys
				365					370					375
Pro	Cys	Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val
				380					385					390
Met	Ala	Pro	Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser
				395					400					405
Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr
				410					415					420
Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro
				425					430					435
Val	Thr	Phe	Pro	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln
				440					445					450
Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro
				455					460					465
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala
				470					475					480
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys
				485					490					495
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp
				500					505					510
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro
				515					520					525
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val



530					535					540				
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly
				545					550					555
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn
				560					565					570
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu
				575					580					585
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe
				590					595					600
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro
				605					610					615
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr
				620					625					630
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser
				635					640					645
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala
				650					655					660
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys
				665					670					675
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly
				680					685					690
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile
				695					700					705
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro
				710					715					720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser
				725					730					735
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu

815

820

825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys  
830 835

&lt;210&gt; 318

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 318

ccctgaagct gccagatggc tcc 23

&lt;210&gt; 319

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 319

ctgtgctctt cggcgcagcc agtc 24

&lt;210&gt; 320

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 320

ccacagatgt ggtactgcct ggggcagtcg gcttgcgcta cag 43

&lt;210&gt; 321

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 321

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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100

ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgttttgga tcttggccct aactctaatt gtctgtttt 200

gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
 gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
 attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
 ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
 aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80					85					90				
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe
				95					100					105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys
				110					115					120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro
				125					130					135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe
				140					145					150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn
				155					160					165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn
				170					175					180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu
				185					190					195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala
				200					205					210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro
				215					220					225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu
				230					235					240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe
				245					250					255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg
				260					265					270
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly
				275					280					285
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys
				290					295					300
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly
				305					310					315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150  
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200  
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250  
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atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100  
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
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Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230	235	

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200

aacccccgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250  
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gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcata 350  
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ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450  
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caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
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tcttattaca gcaacacat tctaggagt ttctgagctc tccactggag 1550  
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atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
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 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
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 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
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 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
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Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
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Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
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Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150



Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155					160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170					175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185					190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200					205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215					220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230					235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
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<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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<211> 225  
<212> PRT  
<213> Homo sapiens

<400> 328

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				20					25					30
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn
				35					40					45
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile
				50					55					60
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met
				80					85					90
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr
				95					100					105
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu
				110					115					120
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile
				125					130					135
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn
				140					145					150
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu
				155					160					165
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala
				170					175					180
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr
				185					190					195
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His
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Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
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<210> 329  
<211> 1315  
<212> DNA  
<213> Homo sapiens

<400> 329

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<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Gly	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
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Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

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Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala	Leu	Met	Cys	Val	Ala	Val	Ala	Leu	Ser	Leu	Ile	Ala	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
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 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150  
 agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200  
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250  
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 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450  
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<210> 334  
<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 334  
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35 40 45  
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
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65 70 75  
Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335  
<211> 742  
<212> DNA  
<213> Homo sapiens

<400> 335  
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gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500  
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tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
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<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
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Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
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Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
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<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
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<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

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				20				25					30	
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35				40					45	

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50						55				60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65						70				75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80						85				90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95						100				105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110						115				120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125						130				135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140						145				150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155						160				165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170						175				180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185						190				195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200						205				210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215						220				225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230						235				240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcacagtc gctgtgactt ggcccagggt ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
 tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400  
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500  
 gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550  
 caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600  
 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
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 ccttcccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750  
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15

Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30

Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45

Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60

Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75

Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90

Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105

Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120

Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg  
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca gccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccggggtaaa gggagggag caattcaatt tgaagtccct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350  
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400  
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttggcaa 450  
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500  
ctccagttcc tectgctgct cctgatgctg ggatgcgtcc tgatgatggt 550  
ggcgatgttg caccctcccc accacacct gcaccagact gtcacagccc 600  
aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650  
tcccaggatt ggggtactgga agctgaggat gagggtgaag agtacagccc 700  
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750  
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cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900  
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tctgtttcca tgatgaggcc tgggtccactc tctgcggaac tgtacacagc 1100  
atcctcgaca cagtgccag ggccttctctg aaggagatca tctcgtgga 1150  
cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200  
ccaggctgga ggggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250

atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300  
 cttcatggat gccactgcg agtgccaccc aggctggctg gagcccctcc 1350  
 tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400  
 gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450  
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 atgtgaggaa ggccctccag tcccccataa gcccacatcag gagccctgtg 1550  
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 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctcttgagc 1850  
 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	
1				5					10					15	
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	



Ala Thr Arg	Ala Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val
				560					565					570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln
				575					580					585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser
				590					595					600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu
				605					610					615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe
				620					625					630
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg						
				635										

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2524

<212> DNA

<213> Homo sapiens

<400> 351

cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50  
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100  
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtgc 200  
caggggaggg ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250  
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 tcggtcatgg tctcgtccca ttccacacca tttgtttctc tgtctccca 1900  
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcactcc 50

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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cgttccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgtga 350  
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccgcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser	1	5	10	15
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu	20	25	30	
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly	35	40	45	
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp	50	55	60	
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser	65	70	75	
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro	80	85	90	
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys	95	100	105	
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala	110	115	120	
Ser																		

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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gtgcctgacg ggggcgctgg cccacggctg tctgcactgc cacagcaact 150  
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tggttggtggc acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggtat ttcccaacg agctgcgaaa 400  
catcttcgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggacc 500  
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
agtagcccc agaggcgctg ggagtgttc caccgccctc ccctgaagtt 600  
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650  
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accctgccca gggccctact gtccctgggg tcccaggctc tccttgagg 850  
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 gggaggcagg ggggtgggga catggagagc tgaggcagcc tcgtctcccc 1800  
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850  
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
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 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
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 ctgcgggatg tgattaaagt cctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln



	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
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Ser Pro Arg Gly Asp Leu Pro					
	155				

<210> 357  
 <211> 1536  
 <212> DNA  
 <213> Homo sapiens

<400> 357  
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 ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc 150  
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 cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250  
 gcatgggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300  
 gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350  
 cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400  
 ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450  
 gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
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 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
 ctctttattc tgggtggacag tggtagaaa gaaaatggga aggtgatatc 650  
 atttttcaaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700  
 ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750  
 catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800  
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850  
 ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
 aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950  
 acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000  
 gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
 tctcttcttc cttcttttaa atttcataac ctcaactcct atccaatttc 1100

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200  
 ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
 tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400  
 cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450  
 tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500  
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20					25					30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35					40					45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50					55					60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65					70					75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80					85					90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95					100					105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110					115					120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125					130					135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140					145					150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155					160					165

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	
				170					175					180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	
				185					190					195	
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser	
				200					205					210	
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr	
				215					220					225	
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val	
				230					235					240	
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly	
				245					250					255	
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys	
				260					265					270	

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

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<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
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agtggctgga cgatggcagc gtccgccgga gccggggcg tgattgcagc 200  
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tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550  
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tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100  
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
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 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
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 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagtggga 1700  
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 cgtggagagt aaaaagtatc gggttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
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Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp		95	100	105
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile		110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys		125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile		140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val		155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr		170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn		185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser		200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly		215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile		230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile		245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn			260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
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agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

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<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
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Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345



Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val  
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

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<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttggtt cattctcctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgacacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
 ctggggcaac cgggctgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgccgggcc gggactgggt cgcgaggggc 200  
 tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250  
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300  
 tcaactgctc ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350  
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
 gcctgtaccg ggtccggatc ccaaggcgac cgggggccct ggatggcctg 450  
 gaagctgggt gctatgtctc ctcttttgc cctgcgtgct ccctgggtgga 500  
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
 tgggtggcggt gtcgggtggt acgcaccccg ggggctgccg gggccatgag 600  
 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650  
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgccctg 700  
 agatggaaca ggcccagaag gccagaacc cccaggagca gaagtccttc 750  
 ttgcgcaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800  
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
 gtgggtgggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
 agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000  
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	
				35					40					45	
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150  
tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200  
ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250  
ctggacttct atcaggtcta ctctctggcc ctggcagctg attggcttca 300  
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350  
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450  
cctcttctcc ctgacttact cactatgctg cttaaccaa ctctctcaag 500  
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550  
ctgctcttct cagccttcga ggctgggtat atccatgagc acgtggaacg 600  
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650  
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700  
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750  
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800  
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ctcctgtcgg accgccgcgt gctgctgctg ggcaccatac aagctctatt 900  
tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950  
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000  
ctgcttggct ctccctgta ccgtatcgcc acctccaaga ggtaccacct 1050  
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100  
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150  
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200  
cagcatgagc ttcttacgga gaaaggatgat ccctgagaca gagcaggctg 1250  
gtgtactcaa ctggttcgg gtacctctgc actcactggc ttgcctaggg 1300  
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400  
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
gaggagccct atgccctga gctgtaacct cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgacttt gtgactgtcc tgtgggttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagttcc 1650  
 ctctgtgtta ctcccattha gaaaataaac acttttaa at gatcaaaaaa 1700  
 aaaaaa 1706

<210> 374  
 <211> 450  
 <212> PRT  
 <213> Homo sapiens

<400> 374  
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 1 5 10 15  
 Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly  
 20 25 30  
 Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe  
 35 40 45  
 Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala  
 50 55 60  
 Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
 65 70 75  
 Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu  
 80 85 90  
 Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
 95 100 105  
 Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu  
 110 115 120  
 Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
 125 130 135  
 Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala  
 140 145 150  
 Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
 155 160 165  
 Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val  
 170 175 180  
 Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
 185 190 195  
 Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu  
 200 205 210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	215	220	225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	230	235	240
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	245	250	255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	260	265	270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	275	280	285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	290	295	300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	305	310	315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	320	325	330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	335	340	345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	350	355	360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	365	370	375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	380	385	390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	395	400	405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	410	415	420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	425	430	435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

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gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tctgtgctctg 100
gctccccgcg tgcgtcgcgg ccacaggctt ccgtatccat gattatttgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaaagg actttggtgg tatctttcac acaaggtatg agcagattca 250
ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcggttggg ccaggagcac ggcgggcggg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500
gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
tttgggcgtt gctaggctga aagggaagcc acaccactgg cttcccttc 800
cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggtt tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

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<210> 376
<211> 188
<212> PRT
<213> Homo sapiens

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<400> 376
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
  1                      5                      10                      15

Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
                      20                      25                      30

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
                      35                      40                      45

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Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr  
                     50                    55                    60  
 Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly  
                     65                    70                    75  
 Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val  
                     80                    85                    90  
 Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln  
                     95                    100                    105  
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp  
                     110                    115                    120  
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg  
                     125                    130                    135  
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr  
                     140                    145                    150  
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile  
                     155                    160                    165  
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu  
                     170                    175                    180  
 Leu Gln Pro Pro Trp Thr Phe Trp  
                     185

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
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 ggctggtggt gatggctggt gtgattccaa tccagggcgg gacacctgaac 100  
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagaccaggg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400



aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15

Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
				35					40					45

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
				50					55					60

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
				65					70					75

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
				80					85					90

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
				95					100					105

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
				110					115	

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 381  
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382  
<211> 764  
<212> DNA  
<213> Homo sapiens

<400> 382  
ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50  
ggcgatgtgg aggggtgccg gcacaaccag acgcccagtc acaggcgaga 100  
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gcccacctg ggcaggggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
gggtgtctgt aggtcttctc ctgggtgaaa gtgtccagggt gaaacttgga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
ctttcctccg gggatatgtc atgtacacca gcaaggaccg ctatttctat 450  
tttggaagc ttgatggcca gatctcctct gcctaccca gccaaagagg 500  
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650  
ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383  
<211> 178  
<212> PRT  
<213> Homo sapiens

<400> 383  
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu  
1 5 10 15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly	
				20					25					30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	
				35					40					45	
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	
				50					55					60	
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	
				65					70					75	
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	
				80					85					90	
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	
				95					100					105	
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	
				110					115					120	
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	
				125					130					135	
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	
				140					145					150	
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	
				155					160					165	
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			
				170					175						

<210> 384  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50  
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100  
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150  
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
 atgttc meta atcggtccat ctcccaaggg gtccaatttt tcttctctggg 400  
 tgtcagcgag ccctgactca ctacagtgcg gctgacaggg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550  
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600  
cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650  
atctcagaaa ttacaggaga taccctcaag tatactgtct ggttgcttag 700  
gtttgtccct tcgtataaac agccttcaaa aacttaagta taatcaattt 750  
aaagggtca accagctcac ctggctatac cttgaccata accatattcag 800  
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950  
gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000  
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
aacctggaac ttttggaact gggatataac cggatccgaa gtttagccag 1100  
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250  
gtcctggacc tggagctcct tacaaaggct tgatttatca ggcaatgaga 1300  
tcgaagcttt cagtggacc agtggtttcc agtgtgtccc gaatctgcag 1350  
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<210> 385  
 <211> 513  
 <212> PRT  
 <213> Homo sapiens

<400> 385  
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 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
 35 40 45  
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
 50 55 60  
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
 65 70 75  
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
 80 85 90  
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
 95 100 105  
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
 110 115 120  
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
 125 130 135  
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
 140 145 150

Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	
				155					160					165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	
				170					175					180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	
				185					190					195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu	
				200					205					210	
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	
				215					220					225	
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	
				230					235					240	
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	
				245					250					255	
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	
				260					265					270	
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	
				275					280					285	
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	
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Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	
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Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	
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Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	
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Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	
				350					355					360	
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu	
				365					370					375	
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu	
				380					385					390	
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly	
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Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile	
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Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu	
				425					430					435	

Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys
				440					445					450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys
				455					460					465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr
				470					475					480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu
				485					490					495
Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
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Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

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<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 388

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<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaata tataatgacc 200  
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taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
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agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
tgagagtgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
ccaacacggg gagaaaagaa aatttccctt ttacagtaa tgaatgtggc 1200  
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cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
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<210> 390
<211> 146
<212> PRT
<213> Homo sapiens
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<400> 390

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Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp
				20					25					30
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln
				35					40					45
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu
				50					55					60
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys
				65					70					75
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala
				80					85					90
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala
				95					100					105
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro
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Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser
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<210> 391
<211> 26
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe

<400> 391

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<210> 392

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

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gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
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<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 395

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				20				25						30	
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu	
				35				40						45	
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu	
				50				55						60	
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser	
				65				70						75	
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu	
				80				85						90	
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp	
				95				100						105	
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr	
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Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val	
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<210> 396  
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<212> DNA  
<213> Homo sapiens

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cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
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<211> 353  
<212> PRT  
<213> Homo sapiens

<400> 397  
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Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser  
35 40 45  
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr  
50 55 60  
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu  
65 70 75  
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp  
80 85 90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe	Ser
95	100	105	
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly	Leu
110	115	120	
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser	Asp
125	130	135	
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser	Ala
140	145	150	
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu	Ser
155	160	165	
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala	Gly
170	175	180	
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn	Arg
185	190	195	
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr	Leu
200	205	210	
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala	Phe
215	220	225	
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu	Gln
230	235	240	
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro	Gly
245	250	255	
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp	Ala
260	265	270	
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu	Asp
275	280	285	
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu	Leu
290	295	300	
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val	Arg
305	310	315	
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro	Gly
320	325	330	
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu	Ser
335	340	345	
Ala Ala Arg Gly	Pro Thr Ile Leu		
350			

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaccccaag cttactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagatc gatttctccc cagtccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtaattc cccaaaaca gttttgacat ttccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550



gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600  
 tgctgcctcc tgcgccatth gctaagactc tatctggaca gggatattta 650  
 aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700  
 ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750  
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 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900  
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
 acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt 1000  
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050  
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 atttttgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150  
 tttttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200  
 ctttaaaaaa attcacagat tatattttata acctgactag agcagggtgat 1250  
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300  
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatcctacac ggccagcatg tttttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	
Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25				30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40				45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	
				50					55					60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	
				65					70					75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	
				80					85					90	
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	
				95					100					105	
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	
				110					115					120	
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	
				125					130					135	
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	
				140					145					150	
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	
				155					160					165	
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	
				170					175					180	
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	
				185					190					195	
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	
				200					205					210	
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	
				215					220					225	
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	
				230					235					240	
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	
				245					250					255	
Trp	Met	Glu	Glu	Thr	Glu										
				260											

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50  
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctaggggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
cacccgccat ttacagacac gtagtgtatt ctggaggtcg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaattggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650  
accacttatg atacagtga aactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtcg agaatgaccc cttggtcaat ggtgttctgg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln	1	5	10	15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	20	25	30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	35	40	45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	50	55	60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	65	70	75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	80	85	90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	95	100	105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	110	115	120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	125	130	135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	140	145	150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	155	160	165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	170	175	180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	185	190	195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	200	205	210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	215	220	225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	230	235	240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	245	250	255	

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr		
	260	265 270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly		
	275	280 285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met		
	290	295 300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg		
	305	310 315
Glu Met Ser Gly Val Ser Pro Phe		
	320	

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgcggatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttggcca gaatgtgaat gtattgactg gaggtagaga 200

agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400  
 ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450  
 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500  
 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550  
 tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650  
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700  
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 ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800  
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850  
 tattcctgag atttagaact tgatctactc cctgagccag gggtacatca 900  
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 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000  
 ttgagggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
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 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150  
 aggttgacgt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200  
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300  
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350  
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400  
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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

gtttgaggaa gctgggatac 20

<210> 412

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccaaactcga gcacctgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

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gcagctggcc cactggcggc ccgcaacact cegtctcacc ctctgggccc 100

actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200

gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250

aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300

acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350

tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450

agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgccagacc 500

aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550

tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600

tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650

ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750

acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800

gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850

cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900

taaagaacag cccagacaca acaaatac agggatggcc agagctgctg 950

gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000

ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050

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gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150

tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200



accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250  
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tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415  
<211> 224  
<212> PRT  
<213> Homo sapiens

<400> 415  
Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala  
1 5 10 15  
Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
20 25 30  
Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
35 40 45  
Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
50 55 60  
Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
65 70 75  
Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
80 85 90  
Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
95 100 105  
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
110 115 120  
Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
125 130 135  
Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
140 145 150  
Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
155 160 165  
Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
170 175 180  
Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
185 190 195  
Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
200 205 210  
Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
215 220

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 416  
gccatagtca cgacatggat g 21  
  
<210> 417  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 417  
ggatggccag agctgctg 18  
  
<210> 418  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 418  
aaagtacaag tgtggcctca tcaagc 26  
  
<210> 419  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 419  
tctgactcct aagtcaggca ggag 24  
  
<210> 420  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 420  
attctctcca cagacagctg gttc 24  
  
<210> 421

<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
gtacaagtgt ggctcatca agcctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
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tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200  
ctctctctct gcctgtccta gtctcttagt cctcaaattc ccagtcccct 250  
gcaccccttc ctgggacact atgttgttct cgcctcctct gctggagggtg 300  
atcttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
cactggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850  
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900

cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
 gacagttttt tatagaagggt cccagatttc aatggaacag ctggaaaagc 1000  
 ttcaggggac attgtttctcc acagaagagg agccctctaa gcttctggta 1050  
 cagaactacc gagcccttca gcctctcaat cagcgcacatg tctttgcttc 1100  
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
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 attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250  
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300  
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 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
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 tttccctaga tatactgagg gatctctcct taggataaag agttgctgtt 1650  
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 t 1701

<210> 423  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 423  
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 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
 20 25 30  
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
 35 40 45  
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
 50 55 60  
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
 65 70 75  
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu  
 80 85 90

Pro Ser Thr Leu Tyr	Leu Gly Gly Leu	Pro Arg Lys Tyr Val	Ala
95		100	105
Ala Gln Leu His	Leu His Trp Gly Gln	Lys Gly Ser Pro Gly	Gly
110		115	120
Ser Glu His Gln	Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu	His
125		130	135
Ile Val His Tyr	Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu	Ala
140		145	150
Ala Glu Arg Pro	Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile	Glu
155		160	165
Val Gly Glu Thr	Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser	His
170		175	180
Leu His Glu Val	Arg His Lys Asp Gln	Lys Thr Ser Val Pro	Pro
185		190	195
Phe Asn Leu Arg	Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr	Phe
200		205	210
Arg Tyr Asn Gly	Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser	Val
215		220	225
Leu Trp Thr Val	Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu	Gln
230		235	240
Leu Glu Lys Leu	Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu	Pro
245		250	255
Ser Lys Leu Leu	Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu	Asn
260		265	270
Gln Arg Met Val	Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser	Tyr
275		280	285
Thr Thr Gly Glu	Met Leu Ser Leu Gly	Val Gly Ile Leu Val	Gly
290		295	300
Cys Leu Cys Leu	Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys	Ile
305		310	315
Arg Lys Lys Arg	Leu Glu Asn Arg Lys	Ser Val Val Phe Thr	Ser
320		325	330
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335			

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 424  
gtaaagtcgc tggccagc 18  
  
<210> 425  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 425  
cccgatctgc ctgctgta 18  
  
<210> 426  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 426  
ctgcactgta tggccattat tgtg 24  
  
<210> 427  
<211> 45  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 427  
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45  
  
<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens  
  
<400> 428  
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acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150  
aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200  
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300

ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350  
 gggttgaatg tacaacagca actgcaccca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
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 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
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 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
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 1 5 10 15  
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys  
 20 25 30  
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75  
 Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn  
 80 85 90  
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro		
	110	115	120
Gln Ile Phe Thr	Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly		
	125	130	135
Ile Leu Pro Thr	Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp		
	140	145	150
Gly Ser Leu Pro	Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln		
	155	160	165
Gly Thr Pro Ala	Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp		
	170	175	180
Asp Phe Ala Val	Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His		
	185	190	195
Ala Ile Glu Glu	Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln		
	200	205	

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgcctct gagatcccca aggggaagca 250
aaaggcgtag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
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aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650
attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

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ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
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ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
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tccaaca 1257

<210> 431  
<211> 243  
<212> PRT  
<213> Homo Sapien

<400> 431  
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20 25 30  
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
35 40 45  
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
50 55 60  
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
65 70 75  
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
80 85 90  
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
95 100 105  
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
110 115 120  
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

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<210> 432

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 432

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<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

cgcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

atgacgctcg tccaaggcca c 21

<210> 435  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 435  
cccacctgta ccaccatgt 19  
  
<210> 436  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 436  
actccaggca ccatctgttc tccc 24  
  
<210> 437  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 437  
aagggctggc attcaagtc 19  
  
<210> 438  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 438  
tgacctggca aaggaagaa 19  
  
<210> 439  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 439  
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<210> 440  
<211> 19

<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
gggtcgtgtt ttggagaga 19

<210> 441  
<211> 20  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 441  
ctggccctca gagcaccaat 20

<210> 442  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 442  
tcctccatca cttcccctag ctcca 25

<210> 443  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
ctggcaggag ttaaagttcc aaga 24

<210> 444  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 445  
agcgtacact ctctccaggc aaccag 26  
  
<210> 446  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 446  
caattctgga tgaggtggta ga 22  
  
<210> 447  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 447  
caggactgag cgcttggtta 20  
  
<210> 448  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
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<400> 448  
caaagcgcca agtaccggac c 21  
  
<210> 449  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 449  
ccagacctca gccaggaa 18  
  
<210> 450  
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<212> DNA  
<213> Artificial Sequence  
  
<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccctagctga ccccttca 18

<210> 451

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 451

tctgacaagc agttttctga atc 23

<210> 452

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 452

ctctccccct cccttttcct ttgttt 26

<210> 453

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 453

ctctggtgcc cacagtga 18

<210> 454

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 454

ccatgcctgc tcagccaaga a 21

<210> 455

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 455  
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<210> 456  
<211> 20  
<212> DNA  
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<220>  
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<400> 456  
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<210> 457  
<211> 22  
<212> DNA  
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<220>  
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<400> 457  
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<210> 458  
<211> 18  
<212> DNA  
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<220>  
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<400> 458  
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<210> 459  
<211> 22  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 459  
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<210> 460  
<211> 23  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 460  
tgctaggcga cgacaccag acc 23

<210> 461  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 461  
  tggacacgtg gcagtgga 18  
  
<210> 462  
<211> 19  
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<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 462  
  tcatggtctc gtccattc 19  
  
<210> 463  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
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  caccatttgt ttctctgtct ccccatc 27  
  
<210> 464  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 464  
  ccggcatcct tggagtag 18  
  
<210> 465  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 465  
  tccccattag cacaggagta 20  
  
<210> 466



<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 466  
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<210> 467  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 467  
gcccagagtc ccacttgt 18

<210> 468  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 468  
actgctccgc ctactacga 19

<210> 469  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 469  
aggcatcctc gccgtcctca 20

<210> 470  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 470  
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<210> 471  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472

tcagggtcta catcagcctc ctgc 24

<210> 473

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

aaggccaagg tgagtccat 19

<210> 474

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

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<210> 475

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 475

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<210> 476

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 476  
gggaggctta taggcccaat ctgg 24

<210> 477  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 477  
ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

-230-

-1-

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B1